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Result
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Maximum Match 100%
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1: /cgn2_6/ptodata/2/paa/PCTUS_COMB.pep:*
2: /cgn2_6/ptodata/2/paa/US06_COMB.pep:*
3: /cgn2_6/ptodata/2/paa/US07_COMB.pep:*
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PCT-US09-303-120B-2
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Sequence 3, Appli
Sequence 3, Appli
Sequence 2, Appli
Sequence 3, Appli
Sequence 2, Appli
Sequence 26292, A
Sequence 5572, Ap
Sequence 6, Appli
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e 20144,	e 9786,	e 5915,	e 576	æ	e 20124,	e 5597,	9155,	Ф		e 4526,	3548,	8329,	e 4476,	e 4814,	e 17137,	æ	2051,	Sequence 26765, A	8725,	8725,	12541,	8207,	820	e 8,	е 8	8, Appl	equence 4464,		4731, A	7,	e 7, Ap	7,	-	Ġ,	Sequence 6, Appli

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0;	Similarity 100.0%; Pred. No. 4.6e-51; Conservative 0; Mismatches 0;	. p.
	Query Match 100:0%; Score 493; DB 1; Length 100;	
	PCT-US00-11473-2	
	; OTHER INFORMATION: Description of Unknown Organism: Microbial ; OTHER INFORMATION: Organism from the human gut	
	; FEATURE:	
	; ORGANISM: Unknown	-
	; TYPE: PRT	
	LENGTH: 100	
	; SEQ ID NO 2	
	; SOFTWARE: Patentin Ver. 2.0	
	; NUMBER OF SEQ ID NOS: 12	
	; PRIOR FILING DATE: 1999-04-30	
	; PRIOR APPLICATION NUMBER: US 09/303,120	
	; CURRENT FILING DATE: 2000-04-28	
	; CURRENT APPLICATION NUMBER: PCT/US00/11473	
	; FILE REFERENCE: FP-PM 4142	
	; TITLE OF INVENTION: Same	
pn	; TITLE OF INVENTION: IBD-Associated Microbial Antigens and Methods of Using	
	; APPLICANT: The Regents of the University of California	
	; GENERAL INFORMATION:	
	; Sequence 2, Application PC/TUS0011473	
	PCT-US00-11473-2	
	RESULT 1	

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.; FEATURE:
.; OTHER INFORMATION: Microbial organism from
PCT-US01-16032A-3

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PCT-US01-16032A-3
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PCT-US01-16032-3
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LENGTH: 100
TYPE: PRT
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CURRENT FILING DATE: 2001-05-17
PRIOR APPLICATION NUMBER: US 09/575,061
PRIOR FILING DATE: 2000-05-19
NUMBER OF SEO ID NOS: 3
SOFTWARE: FastSEO for Windows Version 4.0
SEO ID NO 3
LENGTH: 100
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                                                                                   Query Match
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Best Local Similarity
Matches 100; Conserv
                                                                 Matches 100;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Targan, Stephan R.
APPLICANT: Braun, Jonathan
APPLICANT: Sutton, Christopher L.
TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
TITLE OF INVENTION: Crohn's Disease Using The OmpC Antige
FILE REFERENCE: FP-PM 4713
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SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                   100.0%; Score 493; DB 1; 100.0%; Pred. No. 4.6e-51;
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100.0%; Pred. No. 4.6e-51;
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US-09-575-061-3
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SEQ ID NO 2
LENGTH: 100
TYPE: PRT
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SEQ ID NO 3
LENGTH: 100
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Best Local Similarity 100
Matches 100; Conservative
                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Targan, Stephan R.
APPLICANT: Braun, Jonathan
APPLICANT: Sutton, Christopher L.
TITLE OF INVENTION: Diagnosis, Prevention
TITLE OF INVENTION: Crohn's Disease Using
FILE REFERENCE: P-PM 4097
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CURRENT FILING DATE: 1999-04-30
NUMBER OF SEQ ID NOS: 10
                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/575,061
CURRENT FILING DATE: 2000-05-19
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                                                                                                                                                                                                                              ORGANISM: Unknown
                                                                                                                                                                                                                                                    TYPE: PRT
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                                                                             Conservative
                                                                         100.0%; Score 493; DB 19; 100.0%; Pred. No. 4.6e-51; 7ative 0; Mismatches 0;
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US-09-252-991A-26292
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US-09-820-576-2
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Best Local Similarity
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SEQ ID NO 26292
LENGTH: 245
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Best Local
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LENGTH: 100
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PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
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PRIOR APPLICATION NUMBER: US 09/303,120
PRIOR FILING DATE: 1999-04-30
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TITLE OF INVENTION: IBD-Associated Microbial Nucleic Acid
TITLE OF INVENTION: Molecules
FILE REFERENCE: P-PM 4646
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CURRENT FILING DATE: 2001-03-28
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                                                LQSIMGGSGEAMAVLVYEWRSLSAEBQAHVLALRDVYEQI 100
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NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS APPRIGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                               87.0%;
84.0%;
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No. 8.2e-43;
mana 26292
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RESULT 10
US-09-303-120B-6
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CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 5572
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APPLICANT: Gary L. Breton et al.
APPLICANT: GARY L. BRETON et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTE
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE:
SEQ ID NO 6
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Best Local Similarity
Matches 27; Conserv
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CURRENT APPLICATION NUMBER: PCT/US00/11473
CURRENT FILING DATE: 2000-04-28
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Préd. No. 2.2e-23;
21; Mismatches 25;
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Pred. No. 0.00014;
25; Mismatches 35
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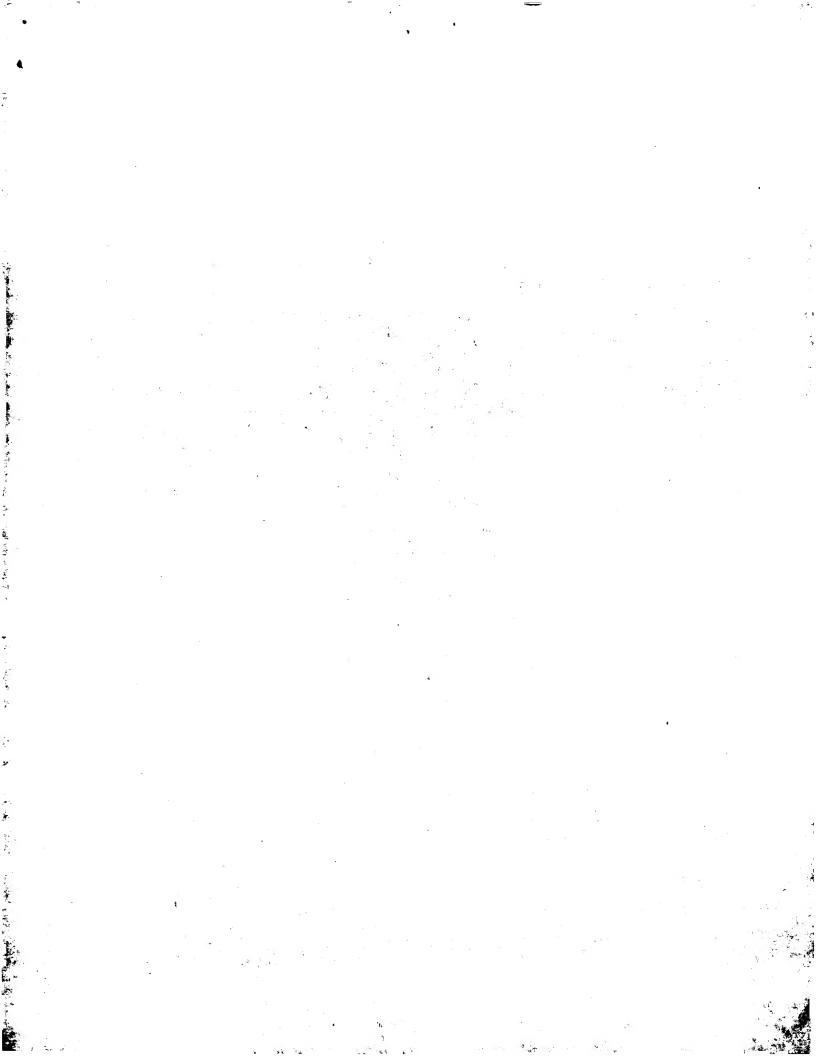
; Sequence 6, Application US/09303120B
; GENERAL INFORMATION:

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RESULT 12
US-09-902-540-14870
Sequence 14870, Application US/09902540
GENERAL INFORMATION:
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CURRENT FILING DATE: 1999-04-30
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
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Best Local
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Best Local :
  APPLICANT:
TITLE OF IN
                                      APPLICANT:
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TITLE OF INVENTION: IBD-Associated Microbial Nucleic Acid
TITLE OF INVENTION: Molecules
FILE REFERENCE: P-PM 4646
CURRENT APPLICATION NUMBER: US/09/820,576
CURRENT FILING DATE: 2001-03-28
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INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
                     Goldman, Barry S.
Hinkle, Gregory J.
Slater, Steven C.
Wiegand, Roger C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Braun, Jonathan
Sutton, Christopher
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                                                                                                                                                                                                                                                                                                                                                                                      22.4%; Score 110.5; DB 22; Length 190; 27.0%; Pred. No. 0.00014; Live 25; Mismatches 35; Indels 13;
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; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 14870
; LENGTH: 202
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Sequence 7, Application PC/TUS0011473
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                                                                                                                                                                                 Sequence 7, Application US/09303120B GENERAL INFORMATION:
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Best Local Similarity
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Best Local
                                                                           APPLICANT: Sutton, Christopher
TITLE OF INVENTION: IBD-Associated Microbial Antigens
TITLE OF INVENTION: Same
FILE REFERENCE: P-PM 3478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: The Regents of the University of California TITLE OF INVENTION: IBD-Associated Microbial Antigens and Methods of Using TITLE OF INVENTION: Same FILE REFERENCE: FP-PM 4142
                  CURRENT APPLICATION NUMBER: US/09/303,120B
CURRENT FILING DATE: 1999-04-30
NUMBER OF SEQ ID NOS: 10
                                                                                                                                           APPLICANT: Braun, Jonathan APPLICANT: Sutton, Christo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US (PRIOR FILING DATE: 1999-04-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: PCT/US00/11473 CURRENT FILING DATE: 2000-04-28
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SOFTWARE:
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TYPE: PRT
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PatentIn Ver. 2.1
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RESULT 15
US-09-820-576-7
Sequence 7, Application US/09820576
GENERAL INFORMATION:
APPLICANT: Braun, Jonathan
APPLICANT: Sutton, Christopher L.
TITLE OF INVENTION: IBD-Associated Microbial Nucleic Acid
TITLE OF INVENTION: Molecules
FILE REFERENCE: P-PM 4646
CURRENT FILING DATE: 2001-03-28
PRIOR APPLICATION NUMBER: US/09/820,576
CURRENT FILING DATE: 2001-03-28
PRIOR FILING DATE: 1999-04-30
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 4.0
SOFTWARE: PastSEQ for Windows Version 4.0
LENGTH: 200
TYPE: PRT
ORGANISM: Mycobacterium tuberculosis
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: LENCTH: 200
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: ORGANISM: Mycobacterium tuberculosis
US-09-303-120B-7
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Best Local Similarity 26.9
Matches 21; Conservative
                                                                                                                          61 LQSIMGGSGEAMAVLVYE 78
                                                                                                    95 FEAIEHHHAQ---VVIYQ 109
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US-09-966-608-2
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US-09-9897-516-4731
US-09-9897-511-2
US-09-9895-6111-2
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US-09-897-516-4814
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US-09-708-427-8313
US-09-708-427-8313
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US-09-708-427-52026
US-09-708-427-52026
US-10-015-127-11169
US-09-708-427-52026
US-10-018-386-5
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67 13.6 187 5 US-09-897-516-6487 Sequence 6487, Ap 66.5 13.5 199 5 US-09-815-242-10.169 Sequence 110169, A 66.5 13.5 349 5 US-09-615-784A-13026 Sequence 13026, A 66.13.4 182 6 US-10-015-127-11354 Sequence 13354, A 66.13.4 219 5 US-09-897-516-7388 Sequence 7388, Ap 65.5 13.3 384 5 US-09-718-427-14867 Sequence 2, Appl. 65.5 13.3 449 5 US-09-708-427-14866 Sequence 14865, A 65.5 13.3 425 5 US-09-708-427-14865 Sequence 14865, A 65.5 13.3 425 5 US-09-708-427-14865 Sequence 14865, A 65.5 13.3 425 5 US-09-708-427-14866 Sequence 14865, A 65.5 13.3 425 5 US-09-708-427-1486 Sequence 14865, A 65.5 13.3 425 5 US-09-708-427-1486 Sequence 14865, A 65.5 13.3 425 5 US-09-708-427-1486 Sequence 7.994, Ap 64.5 13.1 215 7 US-09-897-516-7494 Sequence 69, Appl 64.13.0 233 5 US-09-815-242-5121 Sequence 61, Appl 63.5 12.9 912 7 US-03-33-358-481 Sequence 5121, Ap 63.5 12.9 912 7 US-09-804-693A-64 Sequence 64, Appl 62.5 12.6 219 5 US-09-614-150-1101 Sequence 6101, Appl 62 12.6 219 5 US-09-921-6508-32 Sequence 32, Appl	45	44	43	42	41	40	39	38	37	36	3 5	34	ω ω	32	31	30	29	28	27
187 5 US-09-897-516-6487 Sequence 6487, 199 5 US-09-815-242-10169 Sequence 10166 1826 US-09-675-7848-13026 Sequence 10166 1826 US-09-675-7848-13026 Sequence 11354 Sequence 11354 Sequence 11354 Sequence 11354 Sequence 11354 Sequence 27.84 US-09-897-516-7388 Sequence 27.84 Sequence 27.84 Sequence 14866 Sequence 1521.1 Sequence 1521.1 Sequence 1521.1 Sequence 1521.1 Sequence 1521.1 Sequence 1486.1 Sequence 1521.1 Sequence 1486.1 Sequence	62	62	62.5	63	63.5	64	64	64	64.5	65	65.5	65.5	65.5	65.5	66	66	66.5	66.5	67
5 US-09-897-516-6487 5 US-09-815-242-10169 5 US-09-815-244-10169 5 US-09-75-784A-13026 6 US-10-015-127-11354 6 US-10-015-127-11354 7 US-09-897-516-7388 7 US-09-708-427-14867 7 US-09-708-427-14865 7 US-09-708-427-14865 7 US-09-708-427-14865 8 US-09-708-427-14865 8 US-09-708-427-14865 9 US-09-708-427-14865 9 US-09-708-427-14865 9 US-09-708-427-14865 9 US-09-897-516-7494 9 US-10-015-127-11511 9 US-00-604-693A-64 9 US-00-604-693A-64 9 US-00-604-693A-64 9 US-09-60-337-358-481 9 US-09-604-150-1101 9 US-09-614-150-1101 9 US-09-614-150-1101 9 US-09-921-650B-32 9 Sequence 935, Sequence 32, Market 10	12.6	12.6	12.7	12.8	12.9	13.0	13.0	13.0	13.1	13.2	13.3	13.3	13.3	13.3	13.4	13.4	13.5	13.5	13,6
US-09-897-516-6487 US-09-815-242-10169 US-09-675-784A-13026 US-09-675-784A-13026 US-10-015-127-11354 US-09-897-516-7388 US-09-897-516-7388 US-09-708-427-14867 US-09-708-427-14865 US-09-708-427-14865 US-09-708-427-14865 US-09-708-427-14865 US-09-708-427-14865 US-09-708-427-14865 US-09-708-427-14865 US-09-708-427-14865 US-09-708-427-14865 US-09-60-317-316-69 US-09-815-242-5121 US-09-815-242-5121 US-09-804-693A-64 US-60-337-358-481 US-09-804-198-60 US-09-804-198-60 US-09-614-150-1101 US-09-614-150-1101 US-09-614-150-1101 US-09-614-150-1101 US-09-921-650B-32 US-09-921-650B-32	219	97	1380	350	912	617	233	210	215	957	425	419	384	195	219	182	349	199	187
-09-897-516-6487 Sequence 6487, 109-815-242-10169 Sequence 13026 Sequence 13026-09-675-784A-13026 Sequence 13026-09-675-784A-13026 Sequence 13026-09-675-7848 Sequence 1335-09-897-516-7388 Sequence 2, May 109-708-427-14865 Sequence 14866-09-708-427-14865 Sequence 14866-09-708-427-1494 Sequence 659, Journal of the sequence 5121-09-804-693A-64 Sequence 66, Journal of the sequence 60, Journal of	ű	σ	G	ഗ	7	თ	ഗ	σ	7	σ	5	5	v	ъ	G	σ	5	G	ςı
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			1101	60, 2	481,	64,			69, 1	7494,									

ALIGNMENTS

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RESULT 2
US-09-976-451-5
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                                                                                                                                                                                                                             В
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; SEQ ID NO 2
FMCTH: 100
           Sequence 5, Application US/09976451
GENERAL INFORMATION:
APPLICANT: Braun, Jonathan
APPLICANT: Wei, Bo
APPLICANT: Forbes, Ashley
TITLE OF INVENTION: Methods of Diagnosing and Treating
TITLE OF INVENTION: Crohn's Disease Using Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Applicat GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 100; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Sutton, Christopher L.
TITLE OF INVENTION: IBD-Associated Microbial Nucleic Acid
TITLE OF INVENTION: Molecules
FILE REFERENCE: P-PM 4966
CURRENT APPLICATION NUMBER: US/09/966,608
CURRENT FILING DATE: 2001-09-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Braun, Jonathan APPLICANT: Sutton, Christ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 2001-0: NUMBER OF SEQ ID NOS: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 09/303,120 PRIOR FILING DATE: 1999-04-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 10
TYPE: PRT
FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Unknown FEATURE:
                                                                                                                                                                                                                         _
                                                                                                                                                                                                                                                                                                                        DLASAVGIOSGSIFHHFKSKDEILRAVMEETIHYNTAMMRASLEEASTVRERVLALIRCE 60
                                                                                                                                                                                                                                                                                                    DLASAVGIQSGSIFHHFKSKDEILRAVMEETIHYNTAMMRASLEEASTVRERVLALIRCE 60
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P-PM 4968
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Pred. No. 3.1e-48;
); Mismatches 0;
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               Antigens
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; TYPE: PRT
; ORGANISM: P. fluorescens
US-09-976-451-5
                                                                                                                                                                      US-09-966-608-7
                                                                                                                                                                                            RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0S-09-966-608-6
                                                                                                                               Sequence 7, Application US/09966608 GENERAL INFORMATION:
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CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/240,347
PRIOR FILING DATE: 2000-10-13
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
SEQ ID NO 5
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 190
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GENERAL INFORMATION:
APPLICANT: Braun, Jonathan
APPLICANT: Sutton, Christopher L.
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Best Local Similarity
Matches 27; Conserv
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APPLICANT: Braun, Jonathan
APPLICANT: Sutton, Christopher L.
APPLICANT: Sutton, Christopher L.
TITLE OF INVENTION: IBD-Associated Microbial Nucleic
TITLE OF INVENTION: Molecules
FILE REFERENCE: P-PM 4966
CURRENT APPLICATION NUMBER: US/09/966,608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Sutton, Christopher L.
TITLE OF INVENTION: IBD-Associated Microbial Nucleic
TITLE OF INVENTION: Molecules
FILE REFERENCE: p-pm 4966
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                                                                                                                                                                                                                                                                                               57 IRCELOSIMGGSGEAMAVLVYEWRSLSAEGQAHVLALRDV 96
                                                                                                                                                                                                                                                                                                                                        28 ETASNAGVAKGTLYYHFKSKEEIFKYTTEEGVN----LMKNEIDEATDKEKTALEKLKAV 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40 DLASAVGTQSGSTFHHFKSKDETLRAVMEETTHYNTAMMRASLEEASTVRERVLALTRCK 99
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                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                        25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                      Score 110.5; DB 5;
Pred. No. 6.6e-05;
25; Mismatches 35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 484; DB 5
Pred. No. 8e-47;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 190;
                                                                   Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Acid
                                                                                                                                                                                                                                                                                                                                                                                                                      13; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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; TYPE: PRT ; ORGANISM: Mycobacterium tuberculosis US-09-966-608-7
                                                                                                            RESULT 6
US-09-605-703B-2830
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                                                                Sequence 2830, Application US/09605703B GENERAL INFORMATION:
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SEQ ID NO 4731
LENGTH: 193
TYPE: PRT
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Best Local Similarity 30.6
Matches 33; Conservative
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Matches 21;
APPLICANT: Pompejus, Markus
APPLICANT: Kroger, Burkhard
APPLICANT: Schroder, Hartwi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4731,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Spiridonov, Sergei TITLE OF INVENTION: Xenorhabdus sp. Genome FILE REFERENCE: 38-21(51847)B CURRENT APPLICATION NUMBER: US/09/897,516 CURRENT FILING DATE: 2001-06-29 PRIOR APPLICATION NUMBER: US 60/215, 161 PRIOR FILING DATE: 2000-06-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Goldman, Barry S. APPLICANT: Hinkle, Gregory J. APPLICANT: Huesing, Joseph E. APPLICANT: Krasomil-Osterfeld,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: US 09/303,120
PRIOR FILING DATE: 1999-04-30
PRIOR APPLICATION NUMBER: US 09/820,576
PRIOR FILING DATE: 2001-03-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Corbin, David R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 200
                                                                                                                                                                                                                                             58 R--CELQSIMGGSGEAMAV-LVYEWRSLSAEGQAHVL--ALRDVYEQI 100
                                                                                                                                                                                                                                                                                        31 ELVTAAGVPKGSFYYYFKSKEEFGQILLKE--YFNEYLSRARMLLSSTEGTARERLLNYF 88
                                                                                                                                                                                                      89 RVCSEIQTTGQPEDKCLTVKLGAEVCDLS-EGMRSILCRGTVDIIDQL 135
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                                                                                                                                                                                                                                                                                                                                  1 DLASAVGIQSGSIFHHEKSKDEILRAVMEETIHYNTAMMRASLEEAS---TVRERVLALI 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 DLASAVGIQSGSIFHHFKSKDEILRAVMEETIHYNTAMMRASLEEASTVRERVLALIRCE 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Malvar, Thomas M.
Slater, Steven C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Application US/09897516
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                                                                                                                                                                                                                                                                                                                                                                                                     18.8%; Score 92.5; DB 5 30.6%; Pred. No. 0.0071;
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                                                                                                                                                                                                                                                                                                                                                                              25;
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                                                                                                                                                                                                                                                                                                                                                                                                                            DB 5;
                                                                                                                                                                                                                                                                                                                                                                                     39;
                                                                                                                                                                                                                                                                                                                                                                                                                            Length 193;
                                                                                                                                                                                                                                                                                                                                                                                Indels 11;
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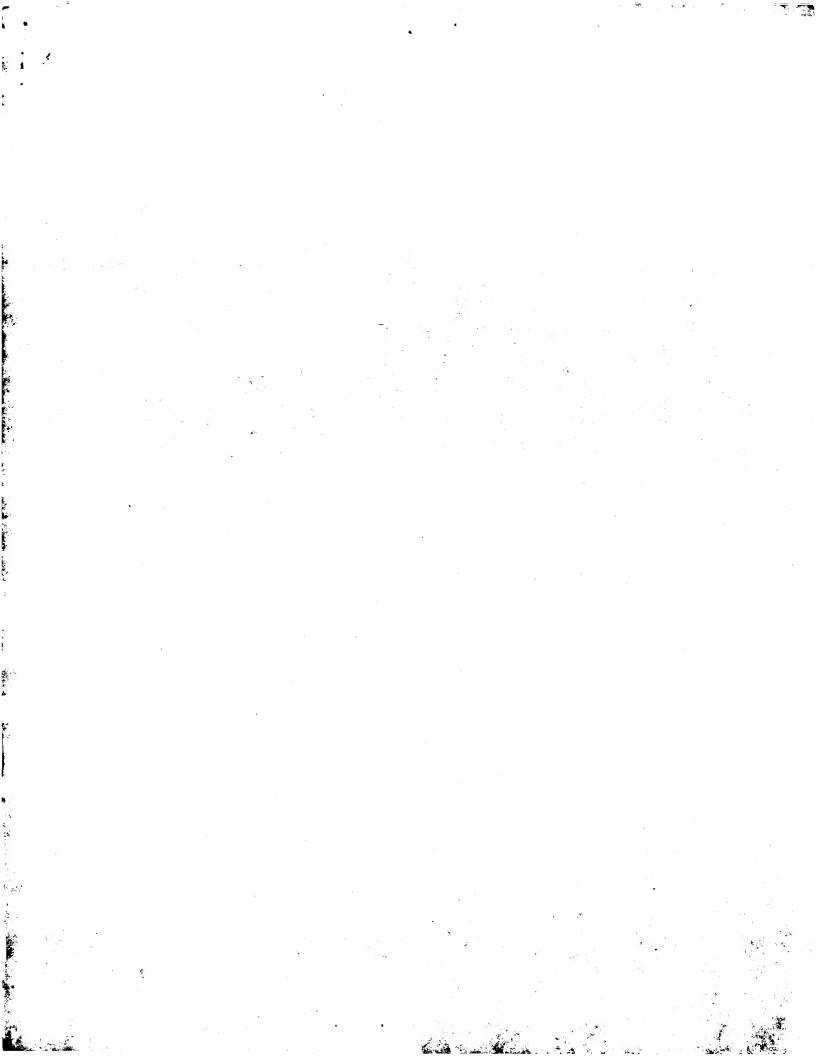
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; TYPE: PRT
; ORGANISM: Aulfex aeolicus
US-09-966-608-8
                                                                                                                            US-08-895-611-2
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US-09-605-703B-2830
                                                                                                                                                 RESULT
                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 41.3
Matches 19; Conservative
                                                              Sequence 2, Application US/08895611
GENERAL INFORMATION:
APPLICANT: DIVERSA CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 8, Application US/09966608 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 18.3
Best Local Similarity 29.4
Matches 20; Conservative
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SEQ ID NO 2830
LENGTH: 218
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Sutton, Christopher L.
TITLE OF INVENTION: IBD-Associated Microbial Nucleic Acid
TITLE OF INVENTION: Molecules
FILE REFERENCE: P-PM 4966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: BGI-129CP
CURRENT APPLICATION NUMBER: US/09/605,703B
CURRENT FILING DATE: 2000-06-27
PRIOR APPLICATION NUMBER: 60/142,764
PRIOR TILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: 60/152,318
PRIOR APPLICATION NUMBER: 60/152,318
PRIOR FILING DATE: 1999-09-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 09/303,120
PRIOR FILING DATE: 1999-04-30
PRIOR APPLICATION NUMBER: US 09/820,576
PRIOR FILING DATE: 2001-03-28
                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/966,608
CURRENT FILING DATE: 2001-09-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Haberhauer, Gregor
TITLE OF INVENTION: CORVNEBACTERIUM GLUTAMICUM GENES ENCODING NOVEL
TITLE OF INVENTION: PROTEINS
                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Braun, Jonathan
                                                                                                                                                                                                             38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97 ASEVRLLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58 RCELQSIM 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41 IADAVGIRQASLYYHFPSKTEIFLTLLKSTVEPSTVL----AEDLSTLDAGPEMRLWAIV 96
                                                                                                                                                                                                         2 LASAVGIQSGSIFHHFKSKDEILRAVMEETIHYNTAMMRASLEEASTV----RERVLALI 57
T: Short, Jay M.
INVENTION: NUCLEOTIDE SEQUENCE OF THE AQUIFEX
                                        Swanson, Ronald V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zelder, Oskar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 104
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                                                                                                                                                                                                                                                                                        18.1%; Score 89; DB 5; Length 192; 41.3%; Pred. No. 0.017; tive 10; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20;
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Pred. No. 0.016;
0; Mismatches 2
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; SOFTWARE: FastSEQ for Windows
; SEQ ID NO 2
; LENGTH: 576775
; TYPE: PRT
; ORGANISM: Aquifex aeolicus
US-08-895-611-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Db 365113 DIAKEVGITEGAIYRHFTSKEEIIKSLLESI----TKELRHKLEVA 365154
; ORGANISM: Aquifex aeolicus US-09-895-611D-2
                                                                                                                                                                                                                                                                                                                                                                                                  US-09-895-611D-2
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                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: DIVERSA CORPORATION
APPLICANT: SWANSON, RONALD V.
APPLICANT: Short, Jay M.
TITLE OF INVENTION: NUCLEOTIDE SEQUENCE OF THE AQUIFEX
TITLE OF INVENTION: ABOLICUS GENOME, FRAGMENTS THEREOF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 18.1
Best Local Similarity 41.3
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/08895611D GENERAL INFORMATION:
                                                                                           SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: I
SEQ ID NO 2
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                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: NUCLEOTIDE SEQUENCE OF THE AQUIFEX TITLE OF INVENTION: AEOLICUS GENOME, FRAGMENTS THEREOFILE REFERENCE: DIVER1330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: DIVERSA CORPORATION APPLICANT: Swanson, Ronald V. APPLICANT: Short, Jay M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/08/895,611
CURRENT FILING DATE: 1997-07-16
NUMBER OF SEQ ID NOS: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: AEOLICUS GENOME, FRAGMENTS THEREOF, AND USES THEREOF FILE REFERENCE: DIVERI330
                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/895,611D CURRENT FILING DATE: 1997-07-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 5 SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/08/895,611D CURRENT FILING DATE: 1997-07-16
                                                                                                                                         NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                         FILE REFERENCE: DIVER1330
                                         LENGTH: 576775
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2, Application US/09895611D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18.1%; Score 89; DB 4; 41.3%; Pred. No. 7.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4; Length 576775;
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US-10-015-127-12199
                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/215, 161
PRIOR FILING DATE: 2000-06-30
NUMBER OF SEQ ID NOS: 8409
SEQ ID NO 4814
LENGTH: 196
                                                                   Matches
                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4814, Application US/09897516 GENERAL INFORMATION:
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Best Local Similarity
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SEQ ID NO 12199
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: Sphingomonas elodea genome sequences and
FILE REFERENCE: 38-10(15806)B
                                                                                                                                                                                                                                                                                                               APPLICANT: Spiridonov, Sergei
TITLE OF INVENTION: Xenorhabdus sp. Genome Sequences And Uses Thereof
FILE REFERENCE: 38-21(51847)B
                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/897,516
CURRENT FILING DATE: 2001-06-29
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CURRENT FILING DATE: 2001-10-29
PRIOR APPLICATION NUMBER: US 60/252,455
PRIOR FILING DATE: 2000-11-22
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                                                                   Local Similarity hes 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35 EICKAAGMSPGNLFHYYPTKNAIIEAIAEEDSHDYDEILAACYDENSVTMTIEKLLA 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
nes 19; Conserv
                               1 DLASAVGIQSGSIFHHFKSKDEILRAVMEETIHYNTAMMRASLEEASTVR--ERVLA 55
                                                                                                                                                                                                                                                                                                                                                                                                       Goldman, Barry S.
Hinkle, Gregory J.
Huesing, Joseph E.
Krasomil-Osterfeld, Karina
                                                                                                                                                                                                                                                                                                                                                                     Malvar, Thomas M. Slater, Steven C.
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                                                                   Conservative
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                                                                                   17.0%;
29.8%;
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                                                                   16;
                                                                                   Score 84; DB 5; Length 196; Pred. No. 0.065;
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                                                                   Mismatches
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                                                                   22;
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                                                                   Indels
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                                                                   Gaps
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US-09-897-516-5915
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; ORCANISM: Xenorhabdus sp.
US-09-897-516-5762
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US-09-897-516-5762
                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 0S 60/215, 161
PRIOR FILING DATE: 2001-06-29
PRIOR FILING DATE: 2000-06-30
NUMBER OF SEQ ID NOS: 8409
SEQ ID NO 5915
LENGTH: 193
TYPE: PRT
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CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/215, 161
PRIOR FILING DATE: 2000-06-30
NUMBER OF SEQ ID NOS: 8409
SEQ ID NO 5762
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                                                                             Matches
                                                                                              Query Match
Best Local Similarity
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APPLICANT: Spiridonov, Sergei
TITLE OF INVENTION: Xenorhabdus sp. Genome
FILE REFERENCE: 38-21(51847)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Corbin, David R. APPLICANT: Goldman, Barry S. APPLICANT: Hinkle, Gregory J. APPLICANT: Huesing, Joseph E. APPLICANT: Krasomil-Osterfeld, APPLICANT: Krasomil-Osterfeld,
                                                                                                                                                                                                                                                                                                                                      APPLICANT: Slater, Steven C.
APPLICANT: Spiridonov, Sergei
TITLE OF INVENTION: Xenorhabdus sp. Genome
FILE REFERENCE: 38-21(51847)B
CURRENT APPLICATION NUMBER: US/09/897,516
CURRENT FILING DATE: 2001-06-29
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35 IAKKAGVSNGIISHYFKDKNKLLEAAMRHLLHQLQMAVARRLRLLDNATPLHRLKAIIEG 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93 RTSVSTFMEFIGHNPNAFRLLLRERSGTSAEFRAAVAREIQHFIAELADYLEQ 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58 RCELQSIM----GGSGEAMAVLVYEWRSLSAEGQA-------HVLA-LRDVYEQ 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40 EVAREAGIAPTSFYRHFRDVDELGLTMVDE----SGLMLRQLMRQA---RQRIAKGGSII 92
                                    2 LASAVGIQSGSIFHHFKSKDEILRAVMEETIH--YNTAMMRASLEEASTVRERVLALIRC 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DLASAVGIQSGSIFHHFKSKDEILRAVMEETIHYNTAMMRASLEEASTVRERVL---ALI 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Goldman, Barry S.
Hinkle, Gregory J.
Huesing, Joseph E.
Krasomil-Osterfeld, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Malvar, Thomas M.
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                                                                             Conservative
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                                                                                              16.18;
27.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23; Mismatches
                                                                             18;
                                                                                              Score 79.5; DB Pred. No. 0.21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Karina C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Karina
                                                                             Mismatches
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                                                                                                                DB 5;
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                                                                           50;
                                                                                                                  Length 193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 183;
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SEQ ID NO 5102
LENGTH: 194
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-815-242-5102
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Search completed: March 4, 2002, 20:31:16 Job time: 399 sec
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US-09-815-242-5102
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CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191.078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
                                                                                                                                                                                                                                                                                                                         Query Match 15.7%; Score 77.5; DB 5; Length 194; Best Local Similarity 25.0%; Pred. No. 0.35; Matches 25; Conservative 23; Mismatches 43; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/269,308 PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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PRIOR FILING DATE: 2000-11-27
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                                                                                                                                                                      60 ELQSIMGGSGEAMAVLVYEWRSLSAE----GQAHVLALRD 95
                                                                                                                         92 WLDNACPPCDEQRCLVV----KLSAEVADLSESMRITLRD 127
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                                                                                                                                                                                                                          32 EILQSAGVPKGSFYHYFKSKEQFGQALLEDYFRVYLADMDQRFSAPGLNARERLMSYWQK 91
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Zyskind, Judith W.
Wall, Daniel
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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493
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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2000 Compugen Ltd.
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267.316 Million cell updates/sec
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Geneseq_1101:* /SIDS2/gcgdata/geneseq/geneseqp/AA1980.DAT:* /SIDS2/gcgdata/geneseq/geneseqp/AA1981.DAT:* /SIDS2/gcgdata/geneseq/geneseqp/AA1982.DAT:* /SIDS2/gcgdata/geneseq/geneseqp/AA1983.DAT:* /SIDS2/gcgdata/geneseq/geneseqp/AA1984.DAT:* /SIDS2/gcgdata/geneseq/geneseqp/AA1985.DAT:* /SIDS2/gcgdata/geneseq/geneseqp/AA1986.DAT:* /SIDS2/gcgdata/geneseq/geneseqp/AA1987.DAT:* /SIDS2/gcgdata/geneseq/geneseqp/AA1989.DAT:* /SIDS2/gcgdata/geneseq/geneseqp/AA1989.DAT:* /SIDS2/gcgdata/geneseq/geneseqp/AA1999.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

13.8 509 21	68 13.8 509 19 AAW47533	14.0 2818 13	14.0	3722 12	15.9 118 21	16.8	18.3	493 100.0 100 21 AAB19839	% Query Score Match Length DB ID	SUMMARIES	Control of annual control of the con
Mouse TIE ligand-3	Amino acid sequenc	• Nf1 gene product.	Virulence dene pro	Cephalosporin anti	Human ORFX ORF289	Streptococcus coel	C glutamicum prote	Inflammatory bowel	Description	ts .	* 5000+0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0

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AAR36783 AAG90850	AAG51228 AAG51227	AAG51229	ААМ4 0856	AAM39070	AAB19432	AAG90819	AAM06441	AAY83794	AAG07352	AAE05486	AAW13280	AAR59922	AAR59921	AAR77223	AAR13895	AAR13753	AAG91263	AAB43299	AAG12674	AAG12675	AAW80943	AAW80941	AAW80938	AAW4 24 28	AAB62490	AAB72902	AAW35389	AAW51254	AAW25747	AAW41604	AAR90296
= 0	Arabidopsis thalia			Human polypeptide	Nucleotide sequenc	amicum	an foeta		Arabidopsis thalia	Human neurofibroma		RAS associated GAP	RAS associated GAP	Tuberous sclerosis		ACVS. Penicillium	C glutamicum prote	0		Arabidopsis thalia	kidney	kidney	~	Glucuronide repres	5	S		proto			Protein having pro

ALIGNMENTS

X P P T	V D D R	γPI	XPA	PR	XX PF	XX	PD X	PN	XX SO	×	Z Z	X	XX	X A	RESULT AAB19839 ID AAB XX
Inflammatory bowel disease (IBD) associated I-2 polypeptides useful diagnosing IBD, vaccinating against IBD and for identifying agents treating IBD - $$	WPI; 2000-687440/67. N-PSDB; AAA89029.	Braun J, Sutton C;	(REGC) UNIV CALIFORNIA.	30-APR-1999; 99US-0303120.	28-APR-2000; 2000WO-US11473.		09-NOV-2000.	WO200066067-A2.	Unidentified microorganism.	Graymosts, vaccing.	I-2; inflammatory bowel disease; IBD; Crohn's disease; therapy; diagnosis: vaccine	Inflammatory bowel disease associated antigen I-2.	05-MAR-2001 (first entry)	AAB19839;	LT 1 9839 AAB19839 standard; Protein; 100 AA.

Inflammatory bowel disease (IBD) associated I-2 polypeptides useful for diagnosing IBD, vaccinating against IBD and for identifying agents for treating IBD - $\,$

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Best Local
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                                                                             Novel polynucleotides derived from Coryneform bacteria, f mutation point of a gene, measuring expression of a gene, expression profile or pattern of a gene and identifying h
     The present inv
sequences from
                                         Claim 17; SEQ ID NO: 4464; 246pp + Sequence Listing; English
                                                                                                                                                                         Nakagawa S,
Tateishi N,
                                                                                                                                                                                                                                                                                                                                                                     Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                              organic acid synthesis
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03-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAG90710 standard; Protein;
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    invention provides rom the Coryneform 1
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Senoh A, Ik
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2000JP-0280988.
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Pred. No. 1.4e-54;
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bacterium
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Corynebacterium
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Best Local
           from Streptomyces coelicolor A3(2), which encodes the MmyR, MmfH, MmfL, MmfR, MmyV, MmyO, MmyJ, and partial Mmr polypeptides. The expression cassette is useful for expressing a nucleic acid of interest, substantially only when the host cell culture reaches high cell density
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention.
                                                                                        9
                                                                                                                                                              Novel expression cassette for expressing a nucleic acid of interest, derived from the regulatory region of methylenomycin gene cluster of SCP1 plasmid of Streptomyces coelicolor A3(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SCP1;
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                                                                                                                                     Claim
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N-PSDB; AAS07627.
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                                                                       sequence represents the MmfR protein encoded by the mmfR gene carried the expression cassette present on plasmid SCP1. The expression sette is the regulatory region of the methylenomycin cluster (mmc)
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MmfR; MmyT; MmyO; MmyG;
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Pred. No. 0.0028;
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MmYJ; Mmr;
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heterologous gene expression
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Best Local
                                                                                                                                                                                                                                              31-MAR-1999;
02-APR-1999;
05-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antiviral; antibacterial; antifungal; antitheumatic; antiinflammatory; antianaemic; gene therapy; cancer; proliferative disorder; hyperten: neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AII cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; ast allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulatio
                                                    Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
                                                                                                                                                                                                                               30-MAR-2000;
                                                                                                                                                                                                                                                                                                          31-MAR-2000;
                                                                                                                                                                                                                                                                                                                                       05-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the system is useful in regulating methylenomycin production. Reduced or no expression of the nucleic acid of interest is observed earlier in growth, avoiding toxic effects of some gene products on growth and the system does not require addition of exogenous inducer. The methylenomycic cluster naturally present on a highly transmissible plasmid permits properly regulated expression in diverse Streptomyces host and the expression is driven by a strong promoter, leading to high yield of the
                                                                                                                                                                                              (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                      WO200058473-A2
                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            vulnerary; antiporiatic; antiparkinsonian; nootropic; neuropro
anticonvulsant; osteopathic; antiarthritic; immunosuppressant;
immunostimulant; thrombolytic; coagulant; vasotropic; antidiab
                                                                                                                                                                                                                                                                                                                                                                                                                               thrombosis; contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; open reading frame; ORFX; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB40525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB40525 standard;
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                                                                                                                       2000-602362/57.
DB; AAC74734.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               end product.
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                                                                                                                                                                                                                                                                                                       2000WO-US08621
                                                                                                                                                                                                                               2000US-0540763
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                                                                                                                                                                                                                                              99US-0127607.
99US-0127636.
99US-0127728.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polypeptide sequence SEQ ID NO:578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16.8%;
42.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 83;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nootropic; neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hepatotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                            coagulation;
                                                                                   frame
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypertension
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        asthma;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AIDS;
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AAC74446 to AAC77606 encode the proteins Claim 11; Page 720; 5507pp; English.

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AAB40237

to AAB43397,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR10145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                         S-(L-alipha-aminoadipyl)-L-cysteinyl-D-; valine synthetase; isopenicillin N synthetase; isopenicillin N epimerase; deacetoxycephalosporin C synthetase; beta-lactamase;
                        Prepn of cephalosporin transformant of microbe
                                                                     WPI; 1991-018854/03
N-PSDB; AAQ10190.
                                                                                                                                              01-FEB-1989;
10-JAN-1990;
                                                                                                                                                                                                                                                                                                               deacetoxycephalosporin C synthetase;
deacetoxycephalosporin C hydroxylase
                                                                                                                                                                                                                                                                                                                                                                            cephalosporin; antibiotic;
                                                                                                                                                                                                                                                                                                                                                                                                           Cephalosporin
                                                                                                                  (TAKE ) TAKEDA CHEMICAL IND KK
                                                                                                                                                                                           10-JAN-1990;
                                                                                                                                                                                                                          03-DEC-1990
                                                                                                                                                                                                                                                        JP02291274-A
                                                                                                                                                                                                                                                                                    Lysobacter lactamgenus
                                                                                                                                                                                                                                                                                                                                                                                                                                         27-MAR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR10145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR10145 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  which represent the human ORFX open reading frames 1 to 3161 sequences have activities such as: cytostatic; hepatotropic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30 elaatagvskpviyehfgskdglyavvvdrevrhlqdslnaamtrpkggpkrtlesavia 89
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                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                       antibiotic biosynthetic enzyme
                                                                                                                                              89JP-0024710.
90JP-0003762.
                                                                                                                                                                                           90JP-0003762
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                 series antibiotics - comprise transformed by plasmid contg.
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Pred. No. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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                                    comprises
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                    s culturing
new DNA
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Best Local S
Matches 20
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See also AAQ10191-2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nakagawa
Tateishi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-APR-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Corynebacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-SEP-2001
                         mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing
                                                                                                                                                                                                                       Claim 17;
                                                                                                                                                                                                                                                                                         expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-DEC-2000; 2000EP-0127688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-JUN-2001
  amino
                                                                                                                  sequences from the Coryneform bacterium Corynebacterium glutamicum. I are useful for identifying the mutation point of a gene derived from
                                                                                                                                              The present invention provides a number sequences from the Coryneform bacterium
                                                                                                                                                                                                                                                                                                                     mutation
                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAH66665
                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-376931/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (KYOW ) KYOWA HAKKO KOGYO KK
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                                                                                                                                                                                                                                                                                         . polynucleotides derived from Coryneform bacteria, for identifying .ton point of a gene, measuring expression of a gene, analysing .ssion profile or pattern of a gene and identifying homologous gene
acids, nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20;
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                                                                                                                                                                                                                     SEQ ID NO: 5200; 246pp + Sequence Listing;
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2000JP-0159162.
2000JP-0280988.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mizoguchi
Senoh A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ando S, Hayashi M,
da M, Ozaki A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 73; pred. No.
       vitamins,
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18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 3722;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ochiai K,
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          producing acids,
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Matches 24
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              virulence gene; antibacterial; vaccine;
septicemia; bronchopneumonia; rhinitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Virulence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB44577 standard; Protein; 80 AA
                                      The family Pasteurellaceae encompasses several pathogens that infect a wide variety of animals. The present invention relates to virulence genes from Pasteurellaceae. The present sequence is a protein encoded by one such virulence gene. The virulence genes of the present invention may be mutated in order to produce an inactive gene. The inactive virulence gene may in turn be used to produce a vaccine, which is useful for treating bacterial infections such as septicemias, bronchopneumonias, rhinitis and
                                                                                                                                                    Claim 39;
                                                                                                                                                                                        Attenuated Pasteurellaceae bacteria comprising mutations in virulence genes, useful as a live attenuated vaccine against bacterial infection
                                                                                                                                                                                                                                                                                                                                                                      06-APR-2000; 2000WO-US09218
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                                                                                                                                                                                                                                                                                                   (PHAA ) PHARMACIA & UPJOHN INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53 VLALIRCELQSIMGGSGEAMAVLVYEWRSLSAE
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                                                                                                                                                   Page 288; 322pp; English
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                                                                                                                                                                                                                                                                          Fuller TE,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  bacterial infection; wound infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This is the amino acid sequence of the von Recklinghausen neuro-fibromatosis (Nfl) gene product. It and antibodies raised to it can be used in hybridisation and immunological assays to screen the presence of a normal or defective Nfl gene product. Function assays to measure levels of gene function can also be used for diagnosis or to monitor treatment. Patient therapy through supplementation with the normal Nfl product which can be produced by recombinant techniques is also possible.
   AAW47533;
                                                                             AAW47533 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1992-041568/05.
N-PSDB; AAQ20602.
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Pred. No. 40;
15; Mismatches
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AAW26792
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Matches 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This is the amino acid sequence of the murine TIE ligand 3, used in the method of the invention, involving the production of TIE-2 ligands which promote healing. The nucleic acids, vectors and host cells used in the method of the invention are useful for the recombinant production of the ligands. The ligands, etc. are useful for blocking blood vessel growth, promoting neovascularisation, promoting the growth or differentiation of a cell expressing the TIE receptor, blocking the growth or differentiation of a cell expressing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chimeric TIE ligand; TIE-2 ligand; neovascularisation; tumour; mouse.
                                                                                                                                           TIE-2 receptor ligand; TIE ligand-3; tyrosine kinase; mouse; angiogenesis; vascularisation; blood vessel growth; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-OCT-1996;
02-AUG-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAV18620
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                                        Mus musculus
                                                                                                      therapy; receptorbody.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13.8%; Score 68; DB 19;
28.4%; Pred. No. 5.2;
Live 18; Mismatches 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This protein comprises novel mouse TIE ligand-3 (mTL-3), a TIE-2 receptor ligand that is a tyrosine kinase with immunoglobulin and epidermal growth factor homology domains. Its amino acid sequence was deduced from an isolated cDNA clone (see AAT99594). A host-vector system for the production of mTL-3 is claimed, as well as an antibody which specifically binds mTL-3, a receptorbody which specifically binds mTL-3, a receptorbody which specifically binds mTL-3 are conjugate comprising mTL-3 and a Cycotoxic agent, and an isolated nucleic acid (see AAT99593) coding C cycotoxic agent, and an isolated nucleic acid (see AAT99593) coding C cycotoxic agent, and an isolated nucleic acid (see AAT99593) coding C cycotoxic agent, and an isolated nucleic acid (see AAT99593) coding C cycotoxic agent, and an isolated nucleic acid (see AAT99593) coding C cycotoxic agent, and an isolated nucleic acid (see AAT99593) coding C cycotoxic agent, and an isolated nucleic acid (see AAT99593) coding C cycotoxic agent, and an isolated nucleic acid (see AAT99593) coding C cycotoxic agent, and an isolated nucleic acid (see AAT99593) coding C cycotoxic agent, and an isolated nucleic acid (see AAT99593) coding C cycotoxic agent, and an isolated nucleic acid (see AAT99593) coding C cycotoxic agent, and an isolated nucleic acid (see AAT99593) coding C cycotoxic agent, and an isolated nucleic acid (see AAT99593) coding C cycotoxic agent, and an isolated nucleic acid (see AAT99593) coding C cycotoxic agent, and an isolated nucleic acid (see AAT99593) coding C cycotoxic agent, and an isolated nucleic acid (see AAT99593) coding C cycotoxic agent, and an isolated nucleic acid (see AAT99593) coding C cycotoxic agent, and an isolated nucleic acid (see AAT99593) coding C cycotoxic agent, and an isolated nucleic acid (see AAT99593) coding C cycotoxic agent, and an isolated nucleic acid (see AAT99593) coding C cycotoxic agent, and an isolated nucleic acid (see AAT99593) coding C cycotoxic agent, and an isolated nucleic acid (see AAT99593) coding C cycotox
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19-JUN-1996;
02-JUL-1996;
                                                                                                                                                                             AR-2 fibrinogen-like domain; angiopoietin related-2; mouse; ischaemia; diabetes; tumour angiogenesis; neoplastic disease; atherosclerosis; thromboembolic disease; inflammatory disease; wound healing; vascularisation; therapy; diagnosis; TIE ligand-3.
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                                     08-SEP-2000
                                                                                     WO200052167-A1
                                                                                                                                     Mus
                                                                                                                                                                                                                                                                                                         Mouse TIE ligand-3 protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY90398 standard; Protein; 509 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            qaqlnslqekreql 232
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96US-0665926.
96US-0021087.
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28.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 68; DB Pred. No. 5.2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence is the mouse Tie ligand-3. This sequence was used in the isolation of the angiopoletin related-2 (AR-2) fibrinogen-like domain (FD) of the invention. AR-2 is useful for treating and diagnosing ischaemia, diabetes, tumour angiogenesis, neoplastic diseases, and for wound healing. The DNA is useful for developing ligands, screening agonists and antagonists of AR-2, and as a therapeutic for treating disorders involving cells, tissues or organs expressing AR-2 receptor. AR-2 is useful to promote the growth, survival, migration, stabilisation or destabilisation, and/or differentiation of cells expressing AR-2 receptor. AR-2 is also useful in assay systems to identify agonists and antagonists of AR-2 receptor. AR-2 is also useful for inducing or preventing vascularisation in diseases or disorders where such function is indicated, for delivering toxins to a receptor bearing cells and as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel nucleic acid molecules encoding fibrinogen-like domain Angiopoietin Related-2 factor useful for treating ischaemia, and for wound healing -
                                            08-JUN-1995;
                                                                                                     W09534659-A1
                                                                                                                                   Arabidopsis sp
                                                                                                                                                               Protoporphyrinogen oxidase; PPO; herbicide; resistance; variegate porphyria.
                                                                                                                                                                                                           Protein having protoporphyrinogen oxidase activity.
                                                                                                                                                                                                                                                                         AAR90296;
                                                                                                                                                                                                                                                                                                      AAR90296 standard; Protein; 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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              16-JUN-1994;
                                                                       21-DEC-1995
                                                                                                                                                                                                                                           02-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            whole body imaging.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diagnostic reagents for detecting the disease by tissue staining or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Fig 1; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jones PF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (REGE-) REGENERON PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                219
                                                                                                                                                                                                                                                                                                                                                                                                                                         165 vlnqtlhmktqmlensl..stnklerqmlmqsrelqrlqgrn...raletrlqaleaqh 218
                                                                                                                                                                                                                                                                                                                                                                                                            87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27 VMEETIHYNTAMMRASLEEASTVRERVLALIRCELQSIMGGSGEAMAVLVYEWRSLSAEG
                                                                                                                                                                                                                                                                                                                                    12
                                                                                                                                                                                                                                                                                                                                                                              qaqlnslqekreql
                                                                                                                                                                                                                                                                                                                                                                                                            QAHVLALRDVYEQI 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000-579286/54.
DB; AAA37838.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Valenzuela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               509 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000WO-US03381
              94US-0261198
                                            95WO-IB00452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 68; DB Pred. No. 5.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                               mutant
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AAW41604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                       21-JUN-1996;
28-FEB-1996;
28-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chimeric gene comprising a promoter (pref. active in a plant) linked to such a DNA or DNA encoding a wild type PPO can be used (1) to impart herbicide resistance to plants; (2) for treating and diagnosing deficient PPO activity in animals (esp. variegate porphyria); and (3) for the production of recombinant PPO which is useful as an assay reagent and in rational design of new inhibitory besteries.
                                                                                                                                                                                                         Arabidopsis thaliana
                                                                                                                                                                                                                                           Protoporphyrinogen oxidase-2; protox-2; herbicide resistance; breeding programmu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      herbicides. Herbicide resistant PPO genes can also be used to select plants transformed with a transgene and probes derived from the genes can be used to quantify levels of PPO mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA encoding eukaryotic proto:porphyrinogen oxidase and herbicide resistant mutants - used to make herbicide resistant plants and
        WPI; 1997-489209/45
N-PSDB; AAV04305.
                                                                                                                                      27-FEB-1997;
                                                                                                                                                              04-SEP-1997
                                                                                                                                                                                  W09732028-A1
                                                                                                                                                                                                                                 genomic mapping.
                                                                                                                                                                                                                                                                              Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                       20-APR-1998
                                                                                                                                                                                                                                                                                                                             AAW41604;
                                                                                                                                                                                                                                                                                                                                                    AAW41604 standard; Protein; 508 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA encoding a modified protoporphyrinogen oxidase (PPO) or a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Volrath
                                            Johnson
                                                                  (NOVS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CIBA ) CIBA
                                                                                                                                                                                                                                                                                                                                                                                                              424
                                                                                                                                                                                                                                                                                                                                                                                                                                                           366 hgfktlgtlfssmmfpdrspsdvhlyttfiggsrnqelakast--delkqvvtsdlqril 423
                                                                                                                                                                                                                                                                                                                                                                                                                                    66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15 HHFKSKDEILRAVM-----EETIHYNTAMMRAS----LEEASTVRERVLALIRCELQSIM 65
                                                                                                                                                                                                                                                                                                                                                                                                             gvegepvsvnhyywr 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1996-049687/05
                                                                                                                                                                                                                                                                                                                                                                                                                           GGSGEAMAVLVYEWR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Page 77-79; 118pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20;
                                          MA,
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                                                                  NOVARTIS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and treatment of variegate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  508 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                            Volrath
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GEIGY
                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                       96US-0020003.
96US-0012705.
96US-0013612.
                                                                                                                                      97WO-US03343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13.7%;
26.7%;
                                                                                                                                                                                                                                                                             protox-2
                                                                                                                                                                                                                                                                                                                                                                                                                                    80
                                          SL,
                                            Ward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 67.5; D
Pred. No. 6;
L6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       English.
                                                                                                                                                                                                                                           programme;
                                            ER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              porphyria
                                                                                                                                                                                                                                                      promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                В
                                                                                                                                                                                                                                            probe;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17;
                                                                                                                                                                                                                                            gene isolation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                508;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JUN-1996;
28-FEB-1996;
28-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protoporphyrinogen oxidase-2 (protox-2).

The protox-1 promoter can be used to express herbicide resistant enzymes, specifically protox, i.e. a plant tissue, plant or progeny containing a chimeric gene of the promoter and a heterologous coding sequence. The plant can also be used in breeding programmes. Also hybridising fragments of the protox coding sequence can be used as probes, e.g. to isolate related genes or for genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA containing a plant proto-porphyrinogen oxidase gene promoter optionally linked to a heterologous gene, especially to express
This protein comprises Arabidopsis protoporphyrinogen oxidase (protox-2), an enzyme that catalyses the oxidation of protoporphyrinogen IX to protoporphyrin IX. Its amino acid s
                                                                                                                                                  New DNA encoding plant protoporphyrinogen oxidase enzyme - and herbicide resistant mutants, useful to prepare plants resistant herbicide which therefore kills undesired vegetation only
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mapping.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  herbicide-resistant enzymes, and plants containing
                                                                                                          Claim
                                                                                                                                                                                                                                                                N'-PSDB; AAT86130
                                                                                                                                                                                                                                                                                     WPI; 1997-448683/41.
                                                                                                                                                                                                                                                                                                                                        Heifetz PB,
                                                                                                                                                                                                                                                                                                                                                                                     (NOVS ) NOVARTIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9732011-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     herbicide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protox-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW25747 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gvegepvsvnhyywr 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGSGEAMAVLVYEWR 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HHFKSKDEILRAVM-----EETIHYNTAMMRAS----LEEASTVRERVLALIRCELQSIM 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hgfktlgtlfssmmfpdrspsdvhlyttfiggsrnqelakast--delkqvvtsdlqrll 423
                                                                                                          95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protoporphyrinogen oxidase; inhibitor;
tolerance; herbicide resistance; trans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pages 43-46;
                                                                                                     Page 102-105; 196pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protoporphyrinogen oxidase (protox-2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                        Johnson
                                                                                                                                                                                                                                                                                                                                                                                                                                     96US-0020003.
96US-0012705.
96US-0013612.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97WO-US03313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13.7%;
26.7%;
                                                                                                                                                                                                                                                                                                                                        MΑ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                114pp; English
                                                                                                                                                                                                                                                                                                                                        Potter SL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     508
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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No. 6;
                                                                                                                                                                                                                                                                                                                                        Volrath SL,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
                                                                                                                                                                                                                                                                                                                                     Ward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  plant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11;
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RESULT 15
AAW51254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
                                             The invention relates to eukaryotic DNA sequences coding for native proto-porphyrinogen oxidase (protox) or modified forms of the enzyme which are herbicide tolerant. Plants having altered protox activity which confers tolerance to herbicides are also provided. These plants
                                                                                                                                                                                                                                         DNA encoding eukaryote herbicide resistant proto-porphyrinogen oxidase - useful for producing recombinant plants having functional enzyme, to be grown in the presence of herbicides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      be expressed in transformed host cells and used tinhibitors of protox enzyme activity, i.e. herbic to design herbicide tolerant forms of the enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  encoding an inhibitor-resistant form of a plant protox enzyme, such as claimed forms from wheat, soybean, cotton, sugarbeet, oilseed rape, rice and sorghum (see AAW25738-48). Application of herbicide will then kill undesired vegetation only. Protox enzymes can also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          was deduced from a previously obtained Protox-1 cDNA clone (see AAT86130). Arabidopsis protox-2 can be modified to render it resistant to protox inhibitors and hence tolerant of certain herbicides. Plants, especially crop plants, may be engineered for resistance to protox inhibitors via mutation of the native protox gene to a resistant form, or they may be transformed with a gene
may be bred or engineered for resistance to protox inhibitors via mutation of the native protox gene to a resistant form or through
                                                                                                                                                                                            Claim 6;
                                                                                                                                                                                                                                                                                                                                                          WPI; 1998-361821/31.
N-PSDB; AAV07252.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-JUN-1995;
16-JUN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proto-porphyrinogen oxidase; protox; herbicide tolerant; resistance;
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US-09-050-663A-4
US-09-0171-296-4
US-09-015-683-4
US-09-015-683-4
US-09-015-683-4
US-09-015-683-4
US-09-191-998-4
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US-09-191-998-2
US-08-222-617A-2
US-08-222-617A-12
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                                                                                                        RESULT
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Best Local Similarity 28.4
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                                   GENERAL INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
TITLE OF INVENTION: Expr
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                          87 QAHVLALRDVYEQI 100
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CITY: Tarrytown
                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
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ZIP: 10591-6707
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STREET: 777 Old Saw Mill River Road
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                                                                                                                                                                                                                                                                                           Score 68; DB Pred. No. 1; 18; Mismatches
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                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                     Sequence 4, Application US/08472028A Patent No. 5767373
                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                      GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Cobert, Robert J
REGISTRATION NUMBER: 36,108
REFERENCE/DOCKET NUMBER: REV
TELECOMMUNICATION INFORMATION:
TELEPHONE: 914-345-7400
                                                                                                                    APPLICANT: Ward, Eric R
APPLICANT: Volrath, Sandra
TITLE OF INVENTION: Manipu
TITLE OF INVENTION: Oxidas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 60/022/999
FILING DATE: 02-AUG-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                            NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                     219 QAQLNSLQEKREQL 232
                                                                                                                                                                                                                                                                                                                                                                   165 VLNQTLHMKTQMLENSL--STNKLERQMLMQSRELQRLQGRN----RALETRLQALEAQH 218
                                              87 QAHVLALRDVYEQI 100
                                                                                                                                                                                                                                                                                                                                                                                     27 VMEETIHYNTAMMRASLEEASTVRERVLALIRCELOSIMGGSGEAMAVLVYEWRSLSAEG 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/0 FILING DATE: 25-OCT-1996
                               STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: 1...509
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Regeneron Pharmaceuticals, STREET: 777 Old Saw Mill Road
                COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
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RY: USA
10532
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                                          Hawthorne
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                                                                          Ciba-Geigy Corporation
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internal
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                                                                                                                         Manipulation of Protoporphyrinogen
Oxidase Enzyme Activity in Eukaryotic Organisms
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Pred. No. 1;
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COMPUTER READABLE FORM:

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US-08-808-931-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No.
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
APPLICANT:
                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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NAME: Elmer, James, Scott
REGISTRATION NUMBER: 36,
                             FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/012,705
FILING DATE: 28-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
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LENGTH: 508 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Heifetz, Peter
TITLE OF INVENTION: DNA Molecules Encoding Plant
TITLE OF INVENTION: Protoporphyrinogen Oxidase a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: 919-541-8614
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           366 HGFKTLGTLFSSMMFPDRSPSDVHLYTTFIGGSRNQELAKAST--DELKQVVTSDLQRLL 423
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                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 10591-9005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15 HHFKSKDEILRAVM-----EETIHYNTAMMRAS----LEEASTVRERVLALIRCELQSIM 65
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REFERENCE/DOCKET NUMBER: CG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/472,028A FILING DATE:
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                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                  STATE:
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                                                                                                                                                                                                                                                                                               Tarrytown
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                                                                                                                                                                                                                                                                                                                EE: No. 5939602artis Corporation 520 White Plains Road, P.O. Box 2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Johnson, Martiner, Sharon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       508 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Volrath, Sandra
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ward, Eric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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26.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                      Protoporphyrinogen Oxidase and Inhibitor-Resistant Mutants
US 60/013,612
                                                                                                                       US/08/808,931
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Pred. No. 1
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Mismatches
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Best Local Similarity
                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/012,705
FILING DATE: 28-FEB-1996
PRIOR APPLICATION UNBER: US 60/013,612
APPLICATION UNBER: US 60/013,612
FILING DATE: 28-FEB-1996
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Johnson, Ma
APPLICANT: Volrath, Sa
APPLICANT: Ward, Eric
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                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
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                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Meigs, J. Timothy REGISTRATION NUMBER: 38,241 REFERENCE/DOCKET NUMBER: CG
                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release "."
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                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15 HHFKSKDEILRAVM-----EETIHYNTAMMRAS----LEEASTVRERVLALIRCELQSIM 65
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                NAME: Meigs, J. Tim
REGISTRATION NUMBER:
                                                                       APPLICATION NUMBER: FILING DATE: 21-JUN
                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: No. 6018105artis Corporation STREET: 520 White Plains Road, P.O. Box 2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGSGEAMAVLVYEWR 80
                                                                                                                                                                                                                                                                                                                                                                                                   10591-9005
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                              J. Timothy
                                                                       JMBER: US 60/020,003
21-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protoporphyrinogen Oxidase Genes
: 26
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26.7%;
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                                                                                                                                                                                                                                                                      US/08/808,323
               38,241
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 CGC 1846
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Pred. No. 1.2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4,
                                                                                                                                                                                        CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/808,931
FILING DATE: 28-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 60/012,705
FILING DATE: 28-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Heifetz, F
TITLE OF INVENTION: I
TITLE OF INVENTION: F
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (919) 541-86 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 2//U3
COMPUTER READABLE FORM:
"""TIM TYPE: Floppy disk
                                            ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,
             TELECOMMUNICATION INFORMATION:
                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
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LENGTH: 508 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS
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                                                                                              APPLICATION NUMBER: FILING DATE: 21-JUI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15 HHFKSKDEILRAVM-----EETIHYNTAMMRAS----LEEASTVRERVLALIRCELQSIM 65
                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE: 30-MA
                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                 REFERENCE/DOCKET NUMBER: CGC 1847
                                                                                                                                                                                                                                                                                                                                                     SOFTWARE:
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TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Heifetz, Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Potter, Sharon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Johnson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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26.7%;
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                                                                                                                                                            us 60/013,612
                                                                                                               us 60/020,003
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                                           38,241
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RESULT 8
US-09-102-420B-4
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Best Local Similarity 26.7%;
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                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/808,931
FILING DATE: 28-FEB-1997
                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0:
FILING DATE: 13-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Heifetz, Peter
TITLE OF INVENTION: HERBICIDE-TOLERANT PROTOPORPHYRINOGEN
TITLE OF INVENTION: OXIDASE ("PROTOX")
                                                                                                                     FILING DATE: 28-FEB-PRIOR APPLICATION DATA:
                                                                                                                                                                         PRIOR APPLICATION DATA:
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OR SAMTON NUMBER: US 60/126,430
                                                                                                                                                                                                                                                                                                                                     FILING DATE: 13-APR-PRIOR APPLICATION DATA:
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                                                                    PRIOR APPLICATION DATA:
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                                                                                  APPLICATION NUMBER: FILING DATE: 28-FE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 11-MAI
                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 09/050,603 FILING DATE: 30-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/0 FILING DATE: 22-JUN-1998 CLASSIFICATION: 800
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                                  FILING DATE:
                                                 APPLICATION NUMBER:
                                                                                                                                                        APPLICATION NUMBER:
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ZIP: 27709
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Research Triangle Park
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                      28-FEB-1996
                                                                                                                                                                                                                                               11-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Floppy disk
                                 JMBER: US 60/020,003
21-JUN-1996
                                                                                                                                          28-FEB-1996
                                                                                                                                                          us 60/012,705
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US 08/472,028
                                                                                                       US 60/013,612
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Pred. No. 1.2;
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TELECOMMUNICATION INFORMATION:

REFERENCE/DOCKET NUMBER: CG

CGC 1847/CIP3

REGISTRATION NUMBER:

Meigs,

J. Timothy

ATTORNEY/AGENT INFORMATION:

FILING DATE:

06-JUN-1995

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US-09-071-296-4
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Best Local Similarity
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                                                     TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
FOR smino acid
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 quence 4, Application US/09071296 tent No. 6177245
                                                                                                                        REFERENCE/DOCKET NUMBER: 36,129
REFERENCE/DOCKET NUMBER: CGC
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                            APPLICATION NUMBER: US 0
FILING DATE: 16-JUN-94
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Manipulation of Protoporphyrinogen
TITLE OF INVENTION: Oxidase Enzyme Activity in Eukaryotic Organisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IUMBER OF SEQUENCES:
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             TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                              NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: 06-JU
                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                              508 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
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06-JUN-1995
protein
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26.7%;
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                                                                                                                                               CGC 1748/CIP
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Pred. No. 1.2;
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Best Local S
Matches 20
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                                                                                                             Matches
                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 0
FILING DATE: 16-JUN-94
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Ciba-Geigy Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Ward, Eric R
APPLICANT: Volrath, Sandra
TITLE OF INVENTION: Manipu
TITLE OF INVENTION: Oxidase
                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
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                                     366
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 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM:
SOFTWARE: PatentI
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les 20; Conserv
                                                                       15 HHFKSKDEILRAVM-----EETIHYNTAMMRAS----LEEASTVRERVLALIRCELQSIM 65
                                                                                                                                                                                                                                       TOPOLOGY:
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                                                                                                                                                                                                                                                                       LENGTH:
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GGSGEAMAVLVYEWR 80
                                     HGFKTLGTLFSSMMFPDRSPSDVHLYTTFIGGSRNQELAKAST--DELKQVVTSDLQRLL 423
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                                                                                                                                                                                                                                                    : 508 amino acids
amino acid
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                                                                                                             Conservative
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SYSTEM: PC-DOS/MS-DOS
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06-JUN-1995
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Oxidase Enzyme Activity in Eukaryotic Organisms
                                                                                                                          13.7%; Score 67.5; D
26.7%; Pred. No. 1.2;
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26.7%; Pred. No. 1.2;
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                                                                                                           Mismatches
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Best Local S
Matches 20
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                   APPLICANT: Ward, Eric R
APPLICANT: Volrath, Sandra
APPLICANT: Volrath, Sandra
TITLE OF INVENTION: Manipulation of Protoporphyrinogen
TITLE OF INVENTION: Oxidase Enzyme Activity in Eukaryotic Organisms
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: CG
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8614
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARRE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/015,683
FILING DATE:
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APPLICANT: Volrath, Sandra
TITLE OF INVENTION: Manipulation of Protoporphyrinogen
TITLE OF INVENTION: Oxidase Enzyme Activity in Eukaryotic Organisms
NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
COMPUTER READABLE FORM:
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CITY: Hawthorne
STATE: NY
                                         COUNTRY:
                                                                                                     STREET:
                                                              STATE:
                                                                                                     ADDRESSEE: Ciba-Geigy Corporation STREET: 7 Skyline Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                             66 GGSGEAMAVLVYEWR 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
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                                                          Hawthorne
: NY
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US-08-449-933-2
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Patent No. 5859195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 13.7%; Score 67.5; D
Best Local Similarity 26.7%; Pred. No. 1.2;
Matches 20; Conservative 16; Mismatches
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 508 amino acids
APPLICATION NUMBER: US/08/44
FILING DATE: 25-MAY-1995
CLASSIFFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KONSK1, ARICOINELE F.
REGISTRATION NUMBER: 34,202
REFERENCE/DOCKET NUMBER: 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 16-JUN-94
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: 919-541-8614
                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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                                                                                                                                                                                                                                                                                   ADDRESSEE: Morrison & Foerster
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 94304-1018
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COMPUTER: IE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wallace,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Marchuk, Douglas A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Collins, Francis S.
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06-JUN-1995
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                                                                                                               US/08/449,933
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                 34,202
   20344-20553.10
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NAME/KEY: Modified-site
LOCATION: group(1264..1290, 1
OTHER INFORMATION: /note= "Mo
OTHER INFORMATION: significan
OTHER INFORMATION: proteins"
FEATURE:
                                                                                                              FEATURE:

NAME/KEY: Modified-site
LOCATION: (1370^1371)
OTHER INFORMATION: /note=
OTHER INFORMATION: insert
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: CDI
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                 NAME/KEY: Modified LOCATION: 1555
OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY: Cleavage-site
LOCATION: group(583..586, 815..818, 2573..2576, 2810..2813)
OTHER INFORMATION: /note= "Potential cAMP-dependent
OTHER INFORMATION: protein kinase recognition sites"
FEATURE:
                                                                                                                                                                                                         NAME/KEY: Modified-site
LOCATION: (2771-2772)
OTHER INFORMATION: /note=
OTHER INFORMATION: acid i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: FEATURE:
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                                                                                                           FEATURE:
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LOCATION: group(1264, 1276, 1358, 1377, 1389, 1390, 1391,
LOCATION: 1395, 1396, 1400, 1423, 1426, 1429, 1430)
OTHER INFORMATION: /note= "Invariant residues within
OTHER INFORMATION: most statistically significant regions
OTHER INFORMATION: GAP family of proteins"
                                                                     NAME/KEY:
LOCATION:
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STRANDEDNESS: si
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(415) 494-0792
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/note= "Most statistically
significant regions of similarity among the
proteins"
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published sequence which shows an ATG methionine
than an ATA isoleucine codon"
                                                                                                                       /note= "Position of a insertion representing
                                                                                                                                                                                                           /note= "Position of an 18 amino acid insertion(SEQ ID NO:10) representing an alternatively spliced product"
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published sequence. Shows an CTG leucine codon rather than
previously published CTC"
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                                                    "NF1 catalytic domain"
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g an alternatively spliced
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US-07-966-049A-2
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COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Applic Patent No. 6238861
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Best Local Similarity
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APPLICANT: Anderson,
APPLICANT: Guttman, I
TITLE OF INVENTION: I
NUMBER OF SEQUENCES:
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PUBLICATION INFORMATION:
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PAGES: 181-186
DATE: 07/13-1990
RELEVANT RESIDUES:
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DATE:
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OTHER INFORMATION:
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OTHER INFORMATION: /note
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VOLUME: 249
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                                                                                                                                                                            Palo Alto
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12/21-1990
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                                                                                                                                                                                                                                                                         Guttman, David H.
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Wallace, Margaret R.
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Version #1.30

Gene

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AUTHORS: Wallace, m.n. c. ....
TITLE: Type 1 Neurofibromatosis Gene:
JOURNAL: Science
                              62 QSIMGGSGEAMAVLVYEW-----RSLSAEGQA
                                                                                                12 SIFHHFKSKDEILRAVMEETIH-----YNTAMMRASLEE-----ASTVRERVLALIRCEL 61
                                                                                                                                                                                                                                                                                                                                          TITLE: Type 1 Neurofibromatosis TITLE: of a Large Transcript in
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EHPTAGNTEAWEDTHAKWEQATKLILNYPKAKMEDGQA
                                                                  SCFRHLCEEADIRCAVDEVSVHNLLPNYNTFMEFASVSNMMSTGRAALQKRVMALLR-RI 766
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                                                                                                                                                      13.6%; Score
26.5%; Pred.
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for the PstI-HindIII fragment designated
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for the HpaI-PstI fragment designated
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for the HpaI-XhoI fragment designated
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CURRENT APPLICATION DATA:

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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141 MRSUNCERS SFO
INFORMATION FOR SEQ ID NO: 2:
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NAME/KEY:
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HYPOTHETICAL:
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OTHER INFO
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OTHER INFORMATION:
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OTHER INFORMATION: /note= "most statistically
OTHER INFORMATION: significant regions of similarit;
OTHER INFORMATION: proteins"
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LOCATION: group(583..586, 815..818, 2573..2576, 2810.
OTHER INFORMATION: /note= "Potential cAMP-dependent
OTHER INFORMATION: protein kinase recognition sites"
                                                                                                                      OTHER INFORMATION:
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STRANDEDNESS: sir
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REGISTRATION NUMBER: 34,207
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group(1264, 1276, 1358, 1377, 1389, 1390, 1391,
1395, 1396, 1400, 1423, 1426, 1429, 1430)
REMATION: /note= "Invariant residues within
REMATION: most statistically significant regions
DEMATION: GAP family of proteins"
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/note= "Position of an 18 amino
acid insertion(SEQ ID NO:10) representing an alternatively
spliced product"
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phosphorylation site"
                                                                                                                  /note= "At variance with previously
published sequence. Lacks an extra CAT histidine condon afte.
this residue"
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                           GENERAL INFORMATION:
APPLICANT: Jefferson, Rich
APPLICANT: Wilson, Katheri
APPLICANT: Leader, Michael
TITLE OF INVENTION: GLUCUF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
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AUTHORS: Wallace, M.R. et al.
TITLE: Type 1 Neurofibromatosis
TITLE: of a Large Transcript in
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AUTHORS: Wallace, M.R. et al.
TITLE: Type 1 Neurofibromatosis Gene: Correction
                                                             NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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OTHER INFORMATION:
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LOCATION:
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VOLUME: 250
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                             3: SEED and BERRY LLP
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for the HpaI-XhoI fragment designated
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for the HpaI-PstI fragment designated pMAL.HF3A.P"
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Pred. No. 17;
18; Mismatches
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COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/882,704A
FILING DATE: 25-UN-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5879906tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 190106.404
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPAX: (206) 682-6031
INFORMATION FOR SEQ. ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 195 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-882-704A-2
                                                                                                                                                                                Query Match 13.3%; Score 65.5; DB 2; Length 195; Best Local Similarity 26.4%; Pred. No. 0.55; Matches 23; Conservative 17; Mismatches 34; Indels 13; Gaps
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Search completed: March 4, 2002, 20:24:35 Job time: 83 sec

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd

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Maximum DB
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493
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400.919 Million cell updates/sec
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ALIGNMENTS

probable transcription regulator PA2885 [imported] - Pseudomonas aeruginosa (strain C;Species: Pseudomonas aeruginosa C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000 σ

C;Accession: C83286
C;Accession: C83286
C;Accession: C83286
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C;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa A;Reference number: A82950; MUID:20437337
A;Accession: C83286

A;Status: preliminary

A; Molecule type: DNA A; Residues: 1-198 <STO>

A:Experimental source: strain PAO1 C:Genetics: A:Gene: PA2885 A;Cross-references: GB:AE004714; GB:AE004091; NID:g9948965; PIDN:AAG06273.1; GSPDB:GN

В Š В δÃ Best Loc Matches Query Match 100 40 Local 1 DLASAVGIQSGSIFHHFKSKDEILRAVMEETIHYNTAMMRASLEEASTVRERVLALIRCE 60 DLASAVGIQSGSIFHHFKSKDEILRSVMEETILYNTALMRAALADAEDLRERVLGLIRCE 99 84; Similarity Conservative 87.0%; 10; Score 429; DB Pred. No. 1.8e 10; Mismatches DB 2; 1.8e-38; 6 Length Indels 0, Gaps 0;

S38906

Appothetical protein 4 - Clostridium pasteurianum C; Species: Clostridium pasteurianum C; Species: Clostridium pasteurianum C; Date: 20 Feb-1995 #sequence_revision 20 Feb-1995 C; Accession: S38906 R; Meyer, J.

submitted to the EMBL Data Library, November 1993 A; Description: Sequence of 6764 bp EcoRI-Sau3A fr 20-Feb-1995 #text_change 08-Oct-1999

Library, November 1993 6764 bp EcoRI-Sau3A fragment of Clostridium pasteurianum

A; Reference number: A; Accession: S38906

A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-190 <MEY>
A;Cross-references: EMBL:Z28353; NID:g431946; PIDN:CAA82211.1; PID:g43:A;Cross-references: EMBL:Z28353; NID:g431946; PIDN:CAA82211.1; PID:g43:C;Superfamily: Bacillus subtilis probable transcription regulator yrhI PID:9431950

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C;Accession: F75281
C;Accession: F75281
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, R;White, O.; Eisen, J.A.; Heidelberg, J.F.; McDonald, L.; Utterback,
C;Genetics:
A;Gene: Rv3557c
                                                                                             A; Molecule type: DNA
A; Residues: 1-200 <COL>
                                                                                                                                      A; Accession: C70604
A; Status: preliminary; nucleic acid
                                                                                                                                                                                           A; Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A; Title: Deciphering the biology of Mycobacterium tuberculosis from the comple A; Reference number: A70500; MUID:98295987
                                                                                                                                                                                                                                                                  Rajandream, M.A.; Ro
Nature 393, 537-544,
                                                                                                                                                                                                                                                                                                                  R;Cole, S.T.; Brosch, R.; Connor, R.; Davies, R.;
                                                                                                                                                                                                                                                                                                                                                                                      probable transcription repressor Rv3557c - Mycobacterium tuberculosis (strain
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
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A; Residues: 1-197 <WHI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski. S.; Smith, H.O.; Venter, J.C.; Fraser, C.M. Science 286, 1571-1577, 1999

A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans
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                                                                    A; Cross-references: GB: Z92774;
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                                                A; Experimental source: strain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Species: Deinococcus radiodurans;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999
                                                                                                                                                                                                                                                                                                                                                                    Accession: C70604
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
les 28; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84 CRVQLNLIYKNRDFFKVIASQLWGK-----ELRQLELRDI 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57 IRCELOSIMGGSGEAMAVLVYEWRSLSAEGQAHVLALRDV 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 DLASAVGIQSGSIFHHFKSKDEIL----RAVMEETIHYNTAMMRASLEEASTVRERVLAL 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 DLASAVGIQSGSIFHHFKSKDEILRAVMEETIHYNTAMMRASLEEAS----TVRERVLAL 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IRCELQSIMGGSGEAMAVLVYEWRSLSAEGQAHVLALRDVYE 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EIASNAGVAKGTLYYHFKSKEEIFKYIIEEGVN----LMKNEIDEATDKEKTALEKLKAV 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IQ-----VVADNMDSATVFFHEWKHLSAEPYAQVVAWRDTID 128
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27; Conser
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                                                                                                                                                                                                                                                                                        Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Ho J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
                                                                      GB:AL123456; NID:g3261729; PIDN:CAB07159.1; PID:e306697;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 110.5; DB 2;
Pred. No. 0.00017;
3; Mismatches 42;
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Pred. No. 0.00016;
                                                                                                                                           sequence not shown;
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R;Kunst, F; Ogasawara, N; Moszer, I; Albertini, A.M.; Alloni, G; Azevedo, V; Ber C; Bron, S; Brouillet, S; Bruschi, C.V.; Caldwell, B; Capuano, V; Carter, N.M.; A; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J; Fabret, C.; Ferrari, Nature 390, 249-256, 1997

A; A; Hosonos; Foulder, D.; Fritz, C.; Fujita, M; Fujita, Y; Fuma, S; Galizzi, A.; Ga
                            A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans A;Reference number: A83650; MUTD:20263314
A;Accession: P84019
                                                                                                                                                                                                                            C; Accession: F84019
                                                                                                                                                                                                                                                                     transcription regulator (TetR/AcrR family) BH2958 [imported] - Bacillus halodurans C;Species: Bacillus halodurans C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 31-Dec-2000
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C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997
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A;Status: preliminary
                                                                                                                                                       Nucleic Acids Res. 28, 4317-4331, 2000
                                                                                                                                                                                            R; Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; GB:AL009126; NID:g2635200; 168
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                                                                                                                                                                                                Sasaki, R.;
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A;Residues: 1-215 <STO>
A;Cross-references: GB:AI
A;Experimental source: st
C;Genetics:
A;Gene: BH2958
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A;Gene:
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C; Access
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C70487
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A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans A;Reference number: A83650; MUID:20263314
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C; Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus A;Reference number: A70300; MUID:98196666
A;Recession: C70487
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transcription regulator TetR/AcrR family - Aquifex aeolicus C; Species: Aquifex aeolicus
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                                                                                              A;Cross-references: GB:AP001517; GB:BA000004; A;Experimental source: strain C-125
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A;Experimental source: strain VF5
                                                                                                                              A; Molecule type: DNA
A; Residues: 1-195 <STO>
                                                                                                                                                            A; Status: preliminary
                                                                                                                                                                              A; Reference number: A; Accession: F84037
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Best I
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;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 17-Mar-2000
;Accession: C70487
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                                                                  BH3102
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19; Conser
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Pred. No. 0.03
LO; Mismatches
 Score
Pred.
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 86;
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0.067;
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0.032;
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A; Residues: 1-197 <S'
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                                                                                                                                                             A; Gene:
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                                                                                                                                                                                                                                           A; Molecule
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                                                                                                                                                                                                                                                                                                                                                                                               probable transcription regulator - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Title: Complete genome sequence of Pseudomonas aeruginosa PA01, A; Reference number: A82950; MUID: 20437337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Stover, C.K.; Pham, X.Q.; adman, S.; Yuan, Y.; Brody, .; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transcription regulator BetI PA5374 [imported] - Pseudomonas aeruginosa (strain C;Species: Pseudomonas aeruginosa C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
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DIAGRAGMSPAALYIHYKTKEELLHRISRIGHTRAVAILRSAAQGEGSAAERLADAVSSF 105
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29.8%;
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Library, July
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L.L.; C
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Pred. No. 0.08
6; Mismatches
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                                                                       Score 84.5; DB Pred. No. 0.11; 2; Mismatches
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1999
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S.N.; Folger,
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K.R.; Kas,
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Larbig,
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probable regulatory protein - Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999 C;Accession: T35424 R;Oliver, K; Harris, D; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajanc submitted to the EMBL Data Library, March 1999 A;Reference number: Z21577 A;Accession: T35424 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-223 <OLI>
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R:Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.: Rarrall B.C. Date.
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                                                   RESULT
D70027
                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Experimental source: strain A3(2) C; Genetics: A; Gene: SCOEDB: SC6A5.33c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: SCOEDB:SC6A5.24c
hypothetical protein yvar - Bacillus C_2Species: Bacillus subtilis
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                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
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                                                                                                                                              104 VESIVLYMAHRRSLAFLDTEIRSLEPANRARYVALRDYLQHM 145
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                                                                                                                                                                                        61 LQSIM--GGSGEAMAVLVYEWRSLSAEGQAHVLALRDVYEQI 100
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                                                                                                                                                                                                                                                                                 1 DLASAVGIQSGSIFHHFKSKDEILRAVMEETIHYNTAMMRASLEEASTVRERVLALIRCE 60
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                                                                                                                                                                                                                                       NIAGRVGVTVPALYYHYENKQALLATLLETSIKDVLDRCRAAAAEAGPA---PLARFCGM 10:
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                                                                                                                                                                                                                                                                                                                                       Conservative
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21.0%;
                                                                                                                                                                                                                                                                                                                                  16.7%; Score 82.5; DB 2; 26.5%; Pred. No. 0.19; tive 24; Mismatches 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                               Length 223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Barrell, B.G.; Rajandream,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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ELQSIMGGS-GEAMAVLVYEWRSLSAEGQAHVLA
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LSSACGLTKASFYHHYPNKEALLRDVLEWT-HQRLAETLFSIAYDPLLTPRERLEKLGRK

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R;Kunst, F; Ogasawara, N; Moszer, I; Albertini, A.M.; Alloni, G; Azevedo, V; Ber C; Bron, S; Brouillet, S; Bruschi, C.V.; Caldwell, B; Capuano, V; Carter, N.M.; A; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, Nature 390, 249-256, 1997

A;Authors: Foulger, D; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galiech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Massuda, S.; Mau y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanl A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiya, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, A; Atthors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtili A; Accession: D70027
A; Carterium Bacillus subtili
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        adman, S.; Yuan, Y.; Brody, L.L.; Lory, S.; Olson, M.V. Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probable transcription regulator PA1241 [imported] - Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Title: Complete genome sequence of Pseudomonas aeruginosa A;Reference number: A82950; MUID:20437337 A;Accession: B83491
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C:Accession: D70027
                                                                                                                                                                                                                                                                                                     A: Experimental source:
                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:AE004553; GB:AE004091; NID:g9947164; PIDN:AAG04630.1; GSPDB:GN
A;Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-186 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Accession: B83491
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A; Residues: 1-190 <KUN>
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                                                                     Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 ELQSI----MGGSGEAMAVLVYEWRSLSA---EGQAHVLALRDVYEQ
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2 LASAVGIOSGSIFHHFKSKDEILRAVMEETIHYNTA--MMRASLEEASTVRERVLALIRC 59
                                                                                                                                                                                                                                             PA1241
                                                              Similarity 28.7
27; Conservative
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                                                                                                        16.2%;
28.7%;
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                                                                                                        Score 80; DB 2; Length 186, Pred. No. 0.28;
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                                                                         Mismatches
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C;Accession: H83274

R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathca; Reference number: A82950; MUID:20437337

A;Accession: H83274
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C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
Search completed: March 4, 2002, 20:25:06 Job time: 94 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Gene: PA2957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: DNA
A;Residues: 1-212 <STO>
A;Cross-references: GB:AE004722; GB:AE004091; NID:g9949054; PIDN:AAG06345.1; GSPDB:GN001
A;Experimental source: strain PAO1
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                                                                                                                                                                                                                                                                                                                                                                          Query Match 16.2%; Score 80; DB 2; Length 212; Best Local Similarity 27.4%; Pred. No. 0.32; Matches 29; Conservative 12; Mismatches 35; Indels
                                                                                                                                                                                                                                                      91 AARLFQDDSIGCLMGVVAVD----ASYGRSELMA 120
                                                                                                                                      99 DPQRYRLFDRLEEKVVKTSQVPEMVE-ELHKIRASNFERLTQLIKE 143
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            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
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Listing first 45 summaries
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"The complete genome sequence of Science 277:1453-1474(1997).
                                                        InterPro; IPR001647; HTH_TetR.
Pfam; PF00440; tetR; 1.
PROSITE; PS01081; HTH_TETR_FAMILY;
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Riley M., Collado-Vides J., Glasner
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Falkenberg
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                                    Repressor;
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                                    Trans-acting factor;
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TRANSCRIPTIONAL
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yhew G.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Davis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R.W.;
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Best Local S
Matches 26
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YY05_MYCTU
Q50720;
Q1-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                    COLE S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Bars. E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., bavies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence."; Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA_BIND
SEQUENCE
                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EWBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and its content is modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                          Nature
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence up
20-AUG-2001 (Rel. 40, Last annotation
HYPOTHETICAL 20.6 KDA PROTEIN RV3405C
RV3405C OR MT3513 OR MTCY78.23
                                                                                                                                                                                                                                                                                                                            Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Rolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MYOSODACTERIUM tuberculosis.

Bacteria; Firmicutes; Actinobacteria; Actinobacteridac
Bacteria; Formnebacterineae; Mycobacteriaceae;
                                                                          EMBL; AE00715;
TIGR; MT3513;
                                                                                                                                        entities requires a license agreement (some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                  Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN-CDC 1551 /
                                                               TubercuList;
                                                                                                           EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=98295987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-H37RV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                              InterPro; IPR001647; Pfam; PF00440; tetR;
                                                                                                                                                                                                                                                                                  laboratory strains.
                                                                                                                                                                                                                                                                                       "Whole genome comparison of laboratory strains.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58
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                                                                                            AE007157;
                                                                                                           Z77165; CAB01018.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 15.3%;
l Similarity 28.6%;
26; Conservative :
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195 AA;
                                                               Rv3405c;
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                                                                                              AAK47851.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed-9634230;
                                                                                                                                                                                                                                                                                                                                                                                             Oshkosh;
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21815
                                                                                                                                                               rmatics Institute. There are no rest
institutions as long as its content
atement is not removed. Usage by an
license are are are allowed.
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                                                                                                                                                                                                                                                                                                 Mycobacterium tuberculosis clinical
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Pred. No. 0.
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; B52A77B3A605E354 CRC64;
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                                                                                                                                                          http://www.isb-sib.ch/announce/
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L outstation -
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Hypothetical PRINTS; PR00455; Pfam; PF00440;

HTHTETR

Complete

YM

(DEGENERATE)

20;

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Gaps

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AVLVYEWRSLSAE

1726 85 Length 2090

(DEGENERATE)

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Best I
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HFC1_MESAU
P51611;
01-OCT-1996
        REPEAT
REPEAT
REPEAT
DOMAIN
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GOLO H., WISHILAHI H., UMENE K.I., NAKADEDU Y., NISHIMOLO T.;
SUDMILITED (FEB-1995) to the EMBL/GenBank/DDBJ databases.
-I. FUNCTION: UPON LYTIC INFECTION OF PERMISSIVE CELLS, THE HSV
TRANSACTIVATOR PROTEIN VP16 ASSOCIATES WITH HCF. BINDING TO HC
ACTIVATES VP16 FOR ASSOCIATION WITH THE OCTAMER MOTIF-BINDING
PROTEIN OCT-1, TO FORM A MULTIPROTEIN-DNA COMPLEX RESPONSIBLE
ACTIVATING TRANSCRIPTION OF THE HSV IMMEDIATE EARLY GENES (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-1996 (rel. 34, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HOST CELL FACTOR C1 (HCF) (VP16 ACCESSORY PROTEIN) (HFC1) (VCAF)
                                                                                     REPEAT
REPEAT
                                                                                                                                                                                                                                                                entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                      SMART;
                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                    InterPro; IPR001777; FN_III.
                                                                                                                                                                                                                   HSSP; P02751; 1FNA
                                                                                                                                                                                                                                  EMBL; D45419; BAA08258.1;
                                                                                                                                                                                                                                                                                              use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                               between
                                                                                                                                                                                                                                                                                                                                                                This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CFF).
                                                                                                                     Nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10036;
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SUBUNIT: COMPOSED PREDOMINANTLY OF SIX POLYPEPTIDES RANGING E SUBUNIT: COMPOSED PREDOMINANTLY OF SIX POLYPEPTIDE. THE MAJORITY ITO 150 KDA AND A MINOR 300 KDA POLYPEPTIDE. THE MAJORITY AND C-TERMINAL CLEAVAGE PRODUCTS REMAIN TIGHTLY, ALBEIT NONCOVALENTLY, ASSOCIATED (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                       PTM: EXISTS AS A FAMILY OF POLYPEPTIDES THAT ARISE THROUGH CLEAVAGE AT ONE OR MORE CENTRALLY LOCATED SITES. CLEAVAGE OCCURS AT A DEFINED SITE, PPCE/THET, WITHIN THE HCF REPEAT (BY
                                                                                                                                                                                                                                                                                                                             European
                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: CONTAINS 5 KELCH REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: NUCLEAR.

DOMAIN: THE HCF REPEAT IS A HIGHLY SPECIFIC
                                                                                                                                                                                                                                                                                                          SWISS-PROT entry is copyright. It is produced through a leen the Swiss Institute of Bioinformatics and the EMBI European Bioinformatics Institute. There are no restrict by non-profit institutions as long as its content is
                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIGNAL (BY SIMILARITY)
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                                                                                                                                    PF00041; fn3; 2.
PF01344; Kelch; 4; SM00060; FN3; 2.
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18; Conserv
                                                                                                                       protein;
                                                                                                                                                                                   IPR001798;
      44
93
148
217
266
1010
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      Repeat.
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194
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1035
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Chordata; Craniata
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                                                                                                                                                                                   Kelch.
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     KELCH 1.
KELCH 3.
KELCH 4.
KELCH 5.
KELCH 5.
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RELCH 5.
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Pred. No. 0.6;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7B226876C5A43630 CRC64
                       AA APPROXIMATE
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                         REPEATS
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STRAIN=K12 / MG1655;
MEDLINE=94089392; PubMed=8265357;
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                                                                                                                                                                                                                                              the European Bioinformatics Institute.
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[2]
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HYPOTHETICAL 24.4
                     Hypothetical CONFLICT
                                                                                  EMBL; AE000470; AAC76945.1; EMBL; X66026; CAA46823.1; AI PIR; S21564; S21564. EcoGene; EG11394; YijC.
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                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=93077482; PubMed=1447162;
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                                                                                                                                                 EMBL; U00006; AAC43069.1; ALT_INIT
                                                                                                                                                                                                                                                                                                                         Sustafsson C., Warne S.R.;
"Physical map of the oxyR-trmA region Escherichia coli chromosome.";
J. Bacteriol. 174:7878-7879(1992).
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$2 PRO 1647; HTH_TetR.

m; PF00440; tetR; 2.

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ALT_INIT.
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Pred. No. 16;
10; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1995
01-NOV-1995
20-AUG-2001
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SEQUENCE
                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBI outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                 influenzae nu. ;
Science 269:496-512(1995).
Science 27071ABTTY: BELONGS TO THE TETR/ACRR FAMILY OF
                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-RD / KW20 / ATCC 51907;
MEDLINE-9530630; PubMed-7542800;
                                                                                           Hypothetical protein; Transcription regulation; DNA-binding;
                                                                                                    PROSITE; PS01081; HTH_TETR_FAMILY; 1.
                                                                                                               Pfam; PF00440; tetR;
                                                                                                                                            EMBL; U32771; AAC22553.1;
                                                                                                                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Bacteria; Proteobacteria;
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            16;
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187 AA;
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                    Score 70; DB 1; Pred. No. 1.6;
                                                             H-T-H MOTIF (BY SIMILARITY).; 53868EF738C024CD CRC64;
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NH34_CAEEL STANDARU;
Q21006;
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30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
NUCLEAR HORMONE RECEPTOR FAMILY MEMBER NHR-34
NHR-34 OR F58GG.5.
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01-FEB-1991 (Rel. 17, Last sequen.
01-MAY-1992 (Rel. 22, Last annota.
HEAT SHOCK COGNATE HSP70 PROTEIN.
Trypanosoma brucei brucei.
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PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
ATP-binding; Heat shock; Multigene family.
SEQUENCE 676 AA; 73694 MW; AD67B783124B785E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in, no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Lee M.G.-S., Polvere R.I., van der Ploeg L.H.T.;
"Evidence for segmental gene conversion between a
and the temperature-sensitively transcribed hsp70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001023; HSP70. Pfam; PF00012; HSP70; 1.
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PIR; A45515; A45515.
HSSP; P19120; 1NGJ.
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SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY
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LAKEANVAAGTIYLYFKNKDELL----EQFAHRVFSMFMATLEK
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Last annotation updat
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7.1;
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7_SYNY3
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15-JUL-1998 (Rel. 3
20-AUG-2001 (Rel. 4
HYPOTHETICAL 28.9 K
SEQUENCE FROM N.A.

MEDLINE-96127529; PubMed-8590279;

Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,

Sugiura M., Tabata S.;

Sugiura M., Tabata S.;

Sequence analysis of the genome of the unicellular cyanobacterium

Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb

region from map positions 64% to 92% of the genome.";

DNA Res. 2:153-166(1995).
                                                                                                                                                                                                                                                           Y617_SYNY3
Q55707;
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SEQUENCE
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                                                                                                                                                       Synechocystis sp.
Bacteria; Cyanoba
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Pfam; PF00105; zf-C4; 1.
PRINTS; PR00047; STROIDFINGER.
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InterPro; IPR001628; zf-C4.
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26.1%;
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Last sequence update)
Last annotation update
PROTEIN SLL0617.
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Pred. No. 5;
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                                                                                                                                                                    PRINTS; PR00455; HTHTETR. FAMILY; 1. PROSITE; PS01081; HTH_TETR_FAMILY; 1.
                                                                                                                                                                                             SubtiList; BG12841; yero.
InterPro; IPR001647; HTH_TetR
Pfam; PF00440; tetR; 1.
                                                                                                                                                                                                                                                                                                                  the
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Submitted (NOV-1997) to
-i- SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacillus subtilis.
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15-JUL-1999 (Rel. 38,
20-AUG-2001 (Rel. 40,
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16; Conser
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26 156 COILED COIL (POTENTIAL).
67 AA; 28905 MW; 5DDE309FFB0FF1A6 CRC64
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the EMBL/GenBank/DDBJ databases
TO THE TETR/ACRR FAMILY OF TRAN
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                                               Score 68.5; D
Pred. No. 3.8;
ll; Mismatches
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Pfam; PF00271; helicase_C; 1.
SMART; SM00487; DEXDc; 1.
SMART; SM00490; HELICC; 1.
SMART; SM00039; DEAD_ATP_HELICASE; FALSE_NEG.
PROSITE; PS00039; DEAD_ATP_HELICASE; FALSE_NEG.
Initiation factor; Protein biosynthesis; ATP-binding; RNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-92051287; PubMed-1719476;

OWLTIM G.W., Hofmann S., Kuhlemeler C.;

"Divergent genes for translation initiation factor eIF-4A are

coordinately expressed in tobacco.";

Nucleic Acids Res. 19:5491-5496(1991).

-I-FUNCTION: EIF-4A IS BOTH A SUBUNIT OF A HIGH MOLECULAR WEIGHT

PROTEIN COMPLEX INVOLVED IN CAP RECOGNITION AND IS REQUIRED AS A

SINGLE POLYPEPTIDE CHAIN FOR MRNA BINDING TO RIBOSOME. IT IS AN

ATP-DEPENDENT SINGLE STRANDED DNA-BINDING PROTEIN WITH A SEQUENCE-

INDEPENDENT UNWINDING ACTIVITY (HELICASE).
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;

Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
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01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
EUKARYOTIC INITIATION FACTOR 4A-3 (EIF-4A-3)
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DNA binding: Helicase: Multigene family.
ATP (BY SIMILARITY).
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InterPro; IPR000629; DEAD_ATP_helcse.
InterPro; IPR001650; Helicase_C.
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                                                                                                                                                                                                                                                                                                                                                                                                                              GIQSGSIFHHFKSKDEILRAVMEETIHYNTAMMRASL-----
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167
391 AA;
(Rel. 35, Created)
(Rel. 35, Last sequence
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                                                                                            STANDARD;
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6.1;
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                                         P39885;
01-FEB-1995
01-FEB-1995
01-NOV-1995
               01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
TETRACENOMYCIN C TRANSCRIPTIONAL REPRESSOR.
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"Genomic structure of a cytoplasmic dynein heavy chain gene from the found of the comparison of the company chain gene from the company chain company chain gene from the nematode Caenorhabditis elegans."

Ceil Motil. Cytoskeleton 32:26-36(1995).

-!- FUNCTION: DYNEIN HAS ATPASE ACTIVITY. CYTOPLASMIC DYNEIN ACTS A MOTOR FOR THE INTRACELLULAR RETROGRADE MOTILITY OF VESICLES AND ORGANELLES ALONG MICROTUBULES.

ORGANELLES ALONG MICROTUBULES.

-!- SUBUNIT: CONSISTS OF AT LEAST TWO HEAVY CHAINS AND A NUMBER OF INTERNEDIATE AND LIGHT CHAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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Rhabditidae; Peloderinae;
                                                                                                                                                                                                                                                                     2165 SGSGKTMA-----WKVLLKALERWENVEGVAHVI 2193
                                                                                                                                                                                                                                                                                                                                                                    2106 IHYTANQMRELRQQLSTVCDEHL-LIYSDVQGEMGSMWLDKVLQLYQITNLNHGLMLVGS 2164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
-1- SIMILARITY: BELONGS TO THE DYNEIN HEAVY CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-96114101;
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                                                                                                                                                                                                                                                                                                                   67 -GSGEAMAVLVYEWRSL-----SAEGQAHVL 91
                                                                                                                                                                                                                                                                                                                                                                                                                     32 IHYNTAMMRASLEEASTVRERVLALIRCELQSIMG-------
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SM00382; AAA; 1.
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R.K., Waterston R.H.;
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COILED COIL (POTENTIAL).
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COILED COIL (POTENTIAL).
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Pred. No. 1.1e+02;
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P (POTENTIAL).
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Best Local S
Matches 33
                                         TSC2_MOUSE STAN
Q61037; Q61007; Q61
20-AUG-2001 (Rel. 4
20-AUG-2001 (Rel. 4
20-AUG-2001 (Rel. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  intergenic operator region.";
J. Bacteriol. 174:3659-3666(1992).
-!- FUNCTION: REPRESSES TRANSCRIPTION OF THE DAND TCMA (TETRACENOMYCIN C RESISTANCE AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=922/004/; runne G.R.;
Guilfoile P.G., Hutchinson C.R.;
"Sequence and transcriptional analysis of the Streptomyces ;
"Sequence and transcriptional C resistance and repressor general control of the Streptomyces in the stranscription of the Streptomyces in the Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaborate between the Swiss Institute of Bioinformatics and the EMBL outstatithe European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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                       TUBERIN (TUBEROUS
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PROSITE; PS01081; HTH_TETR_FAMILY; 1.
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PIR; S27686; S27686.
InterPro; IPRO01647; HTH_TetR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TO AN INTERGENIC OPERATOR REGION. TETRACENOMYCIN C.
                                                                                                                                                                                                                                                                                                                                                                                          IAEAVEVHPRTFFRHFASKEEVALTPISAIDE-----AFLAALEVRPAGENPLQAMSG
                                                                                                                                                                                                                                                                                                               VRERVLALIR-CELQSIMGGSGEAMAVLV----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
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               STANDARD; PRT; 1814 AA.; Q61008; P97723; P97724; P97725 el. 40, Created) el. 40, Last sequence update) el. 40, Last annotation update) ous SCLEROSIS 2 HOMOLOG PROTEIN)
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28.0%;
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Pred. No. 3
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                                                                                                                   4 AA.
P97725;
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                                                                                                                   Q9WUF6
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EMBL: U37775; AAA86902.1; -. EMBL: U37775; AAA86901.1; -. EMBL: U39818; AAB18754.1; -. EMBL: AB009371; BAAA8845.1; -EMBL: AF132986; AAD27867.1; -- MGD: MGB: 102548; TSC2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kleymenova E.V., Declue J.E., Walker C.L.;

Kleymenova E.V., Declue J.E., Walker C.L.;

"Genetic variants of the tuberous sclerosis 2 tumour suppressor gene in mouse t haplotypes.";

Genet. Res. 74:139-144(1999).

-i- FUNCTION: IMPLICATED AS A TUMOR SUPPRESSOR. MAY HAVE A FUNCTION IN VESICULAR TRANSPORT, BUT MAY ALSO PLAY A ROLE IN THE REGULATION OF TRANSCRIPTION MEDIATED BY STEROID RECEPTORS. INTERACTION BETWEEN HAWARTIN AND TUBERIN MAY FACILITATE VESICULAR DOCKING. SPECIFICALLY STIMULATES THE INTENNS. SUGGESTING A POSSIBLE MECHANISM FOR ITS ROLE IN REGULATING RABS. SUGGESTING A POSSIBLE MECHANISM FOR ITS ROLE IN REGULATING CELLULAR GROWTH (BY SIMILARITY).
EMBL; AF13296; AAD27867.1; -.

MGD; MGI:102548; Tsc2.

InterPro; IFR000331; Rap_GAP.

InterPro; IFR003913; Tuberin.

Pfam; PF02145; Rap_GAP; 1.

Anti-oncogene; Alternative splicing; GTPase activation.

VARSPLIC

79

115

MISSING (IN ISOFORM A).

VARSPLIC

534

572

MISSING (IN ISOFORM B).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sarker A.H., Ikeda S., Nakano H., Terato H., Ide H. Akiyana K., Tsutsui K., Bo Z., Kubo K., Yamamoto K. Yoshida M.C., Seki S.;
"Cloning and characterization of a mouse homologue Escherichia coli endonuclease III.";
J. Mol. Biol. 282:761-774(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=96258425; PubMed=8777431;
Kim K.K., Pajak L., Wang H., Field L.J.;
"Cloning, developmental expression, and evidence
splicing of the murine tuberous sclerosis (TSC2)
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                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ASSOCIATION WITH MEMBRANES (BY SIMILARITY). ALTERNATIVE PRODUCTS: 7 ISOFORMS; A, B, C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADAPTER MOLECULE RABAPTIN 5. THE FINAL COMPLEX CONTAINS AND RABAPTIN 5 LINKED TO RAB5 (BY SIMILARITY).
SUBCELLULAR LOCATION: CYTOPLASMIC. AT STEADY STATE FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HERE); ARE PRODUCED BY ALTERNATIVE SPLICING. TISSUE SPECIFICITY: WIDELY EXPRESSED.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pean Bioinformatics Institute. There are no restrictions non-profit institutions as long as its content is in and this statement is not removed. Usage by and for contents the statement is not removed.
                                                                                                                                                                                                                                                                                            AAA86901.1; -.
AAB18754.1; -.
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TSC2 homolog.
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Yasui A.,
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Best Local Similarity 27.5%;
Matches 25; Conservative 1
                                                                                                                                                                                                                                                                                   Pan W., Spratt B.G.;
"Regulation of the permeability of the gond the mtr system.";
Mol. Microbiol. 11:769-775(1994).
-!- FUNCTION: PUTATIVE REPRESSOR OF MTRC GE PERMEABILITY OF THE CELL ENVELOPE TO HY ANTIBIOTICS AND DETERGENTS.
-!- SIMILARITY: BELONGS TO THE TETR/ACRR FA REGULATORS.
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Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
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REGULATORY PROTEIN MTRR.
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17; Mismatches
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MISSING (IN REF. 2).
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A -> N (IN REF. 2).
I -> N (IN REF. 2).
D -> N (IN REF. 2).
C -> AA (IN REF. 2).
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GHAPVQVIVSATGC -> RDTALYKSLSVPAAG (IN ISOFORM E AND ISOFORM F).
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                                                                                                                                                   Matches
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Best Local Similarity
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PROSITE; PS01081; HTH_TETR_FAMILY; 1.

Transcription regulation; DNA-binding; Repressor.

DNA_BIND 32 51 H--Y (IN PENICILLIN-RESISTANT VARIANT 105 105 H -> Y (IN PENICILLIN-RESISTANT ISOLATES).

SEQUENCE 210 AA; 24192 MW; 41E26446CBEF57F2 CRC64;
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                                                                                                                DDLDKETAVIFIKSTLDGLIWRWFS 179
                         GGSGEAMAV-----LVYEWRS
                                                FFERLQSNDIHYKFHNILFLKCEHTEQNAAVIAIARKHQAIWREKITAVLTEAVENQDLA 154
                                                                                                 EIAQAAGVTRGALYWHFKNKEDLFDALFQRICDDIENCIAQDAADAEGGSWTVFRHTLLH
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Search completed: March 4, 2002, 20:28:54 Job time: 97 sec

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Copyright (c) 1993 - 2000 Compugen Ltd
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Q9hzw2 pseudomonas
Q59306 clostridium
Q9rrv9 deinococcus
P96839 mycobacteri
P94548
Q9x8p5
Q9x8p5
Q9a314
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Q9k394
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	09w1r3	Q912q9	Q9aiq9	007388	Q9s2v6	Q9aa74	Q9s250	Q9kxt8	Q9x8m4	Q9zgb7	087854	Q9jv29	Q9a250	Q9s261	Q9k017	Q9a690	Q9a9q5	066658	Q9i1s1	053165	Q9k3m6	Q9a905	Q9rmy4	Q9xa31	Q9hzp1	091497
-	drosophila	pseudomonas	staphylococ	mycobacteri	streptomyce	caulobacter	streptomyce	streptomyce	streptomyce	streptomyce	streptomyce	neisseria m	caulobacter	streptomyce	neisseria m	caulobacter	caulobacter	aquifex aeo	pseudomonas	mycobacteri	streptomyce	caulobacter	bacillus an	streptomyce	pseudomonas	pseudomonas

ALIGNMENTS

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Query Match 98.2%; Score 484; DB 2; Length 207; Best Local Similarity 98.0%; Pred. No. 2.7e-42; Matches 98; Conservative 1; Mismatches 1; Indels 0; Gaps 0;	QSRFR4 OPREMA COPERRA COPER	RESULT 1

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4 streptomyce
4 bacillus ha
6 pseudomonas
5 streptomyce
6 streptomyce
9 streptomyce
9 streptomyce
6 streptomyce
6 caulobacter
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corynebacte

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RESULT
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Q59306;
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01-NOV-1996 (TrEMBLrel. 01, L
01-JUN-2001 (TrEMBLrel. 17, L
30S RIBOSOMAL PROTEIN S21.
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Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M. Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Brody L.L., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.;
"Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen.";
Nature 406:999-964 (2000).
                   Meyer J.;
Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PRO0455; HTHTETR.
PROSITE; PS01081; HTH TETR_FAMILY; 1.
Complete proteome; DNA-binding; Transcription regulation.
SEQUENCE 198 AA; 22057 MW; 079217CCC7B8FF85 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2001 (TERMBLEEL 16, Created)
01-MAR-2001 (TERMBLEEL 16, Last sequence up
01-JUN-2001 (TERMBLEEL 17, Last annotation
PROBABLE TRANSCRIPTIONAL REGULATOR.
                                                                                                                                                           Clostridium.
NCBI_TaxID=1501;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: TO THE TETR/ACRR FAMILY OF EMBL; AE004714; AAG06273.1; -. Interpro; IPR001647; HTH_TetR.
Pfam; PF00440; tetR; 1.
                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                 Bacteria;
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Pred. No. 1.2e-36;
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RESULT P96839

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RESULT
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Best Local :
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Best Local :
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01-MAY-2000
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-20036896; PubMed-10567266; White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D., White O., Eisen D.H., Heidelberg J.F., Hickey E.K., Richardson D.L., Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L., Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C., Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D. Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C., Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Deinococcus radiodurans.

Bacteria; Thermus/Deinococcus group; Deinococcales; NCBI_TaxID=1299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: TO THE TETR/ACRR FAMILY OF TRANSCRIPTION/
EMBL; 228353; CAA82211.1; -:
Interpro; IPR001647; HTH_TetR.
Pfam: PF00440; tetR; 1.
PROSITE; PS01081; HTH_TETR_FAMILY; 1.
DNA-binding; Ribosomal protein; Transcription regulation.
DNA-binding; Ribosomal protein; Oc6ED92A48AA69C0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001647; HTH_TetR. Pfam; PF00440; tetR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9RRV9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9RRV9
                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00455; HTHTETR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.";
  92
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                                                                                                                                                                 1 DLASAVGIQSGSIFHHFKSKDEIL----RAVMEETIHYNTAMMRASLEEASTVRERVLAL 56
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                               IRCELQSIMGGSGEAMAVLVYEWRSLSAEGQAHVLALRDVYE
                                                                                                             DLAGQLGMQGGSLYAHISGKEELLVEIVRGASQQFDEALFSLRDVNLPADEKLREAMFRH
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IQ-----VVADNMDSATVFFHEWKHLSAEPYAQVVAWRDTID
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27; Conserv
                                                                                                                                                                                                                                                        Similarity
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197 AA; 22307 MW; 769F2960C53F848D CRC64;
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(TremBLrel. 13, Last sequence up)
(TremBLrel. 17, Last annotation
                                                                                                                                                                                                                              Conservative
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Pred. No. 0.
                                                                                                                                                                                                                                                        Score 110.5; DB 2
Pred. No. 0.00088;
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Best Local
                                                                                                            SEQUENCE FROM N.A.

MEDLINE-97217425; PubMed-9063446;
Goethel S.F., Schmid R., Wipat A., Carter
Harwood C.R., Marahiel M.A.;
"An internal FK506-binding domain is the
                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-1997 (TrEMBLrel.
01-JAN-1998 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Deciphering the biology of Mycobacterium tuberculosis from complete genome sequence.";
Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=98295987; PubMed=9634230; Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harr. Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Gordon S.V., Basham D., Brown D., Chillingworth T., Connor R., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Sqares R., Sulston Taylor K., Whitehead S., Barrell B.G.,
                                                                                                                                                                                                                                                        Bacteria; Firmicutes; Bacillus/Staphylococcus NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: TO THE TETR/ACRR EMBL; Z92774; CAB07159.1; -. Tuberculist; Rv3557c; -.
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01-MAY-1997 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                Bacillus subtilis
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SEQUENCE 200 AA; 22906 MW; E1B29D39CF4D955F CRC64
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Bacteria; Firmicutes; Actinobacteria;
  SEQUENCE FROM
                                            Eur 350 Biochem. 244:59-65(1997)
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26.9%;
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01-OCT-2000 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
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-!- SIMILARITY: TO THE TETR/ACRR FAMILY OF TRANSCRIPTIONAL REGULATORS EMBL; Z75208; CAA99572.1; --
EMBL; Z99118; CAB14815.1; --
                                          BH2958.
Bacillus halodurans
                                                                                                                           TRANSCRIPTIONAL
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27.4%;
Bacillus/Clostridium group,
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^^r 'TETR/ACRR FAMILY).
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01-JUN-2001 (TrEMBLrel. 17, Last sequen
01-JUN-2001 (TrEMBLrel. 17, Last annota
                                                                                                                                                                                                                                Complete
SEQUENCE
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-I- SIMILARITY: TO THE TETR/ACRR FAMILY OF TRANSCRIPTIONAL EMBL; AP001517; BAB06677.1:
-InterPro; IPR001647; HTH_TetR.
Pfam; PF00440; tetR; 1.
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Fuji F., Hirama C., Nakamura Y., O
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MEDLINE=20512582; PubMed=11058132;
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NCBI_TaxID=86665;
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                                                                                                                           Local Similarity
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                                                                                                                              Pred.
                                                                                                                           Score 90; DB 2; Pred. No. 0.11;
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, Ogasawara
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Best Local
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067927;
01-AUG-1998
01-AUG-1998
01-JUN-2001
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Q9S3L4;
Q1-MAY-2000
Q1-MAY-2000
Q1-JUN-2001
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                                                                                                                                                                                                                            01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
TRANSCRIPTIONAL REGULATOR (TETR/ACRR FAMILY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Corynebacterium glutamicum (Brevibacterium flavum).
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Corynebacteriaceae;
Nature 392:353-358(1998).
-|- SIMILARITY: TO THE TETR/ACRR
EMBL, AE000776; AAC07881.1; -.
InterPro; IPR002106; AA_tRNA_liga
                                                       aeolicus
                                                                Deckert G., Warren P.V., Gaasterland T., Young W.G., Graham D.E., Overbeek R., Snead M.A., Keller M., Auj. Feldman R.A., Short J.M., Olson G.J., Swanson R.V.; "The complete genome of the hyperthermophilic bacter
                                                                                                                                                                                      Aquifex aeolicus.
Bacteria; Aquificales;
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                                                                                                                      MEDLINE=98196666; PubMed=9537320;
                                                                                                                                     STRAIN-VF5
                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PRO0455; HTHTETR.

DNA-binding; Transcription regulation.

SEQUENCE 222 AA; 24381 MW; 5A716AA0E957FFB3 CRC64.
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                                                               "The complete
                                                                                                                                                                         NCBI_TaxID=63363;
                                                                                                                                                                                                                ACRR2 OR AQ_2179.
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  AA_tRNA_ligase_II
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Last sequence update)
Last annotation updat
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Pred. No. 0.13
20; Mismatches
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IPR001647; HTH_TetR

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RESULT
Q9K8A4
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AC Q9
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Best Local S
Matches 19
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Best Local Similarity
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Q9K8A4
Q9K8A4;
01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                  Redenbach M., Kieser H.M., Denapaite D., Eichner A Kinashi H., Hopwood D.A.;

"A set of ordered cosmids and a detailed genetic a the 8 Mb Streptomyces coelicolor A3(2) chromosome.

Mol. Microbiol. 21:77-96(1996).

-- SIMILARITY: TO THE TETR/ACRR FAMILY OF TRANSCR EMBL; AL360034; CAB95981.1;

InterPro: IPR001647; HTH_TetR.

Pfam: PF00440; tetR: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PUTATIVE TETR-FAMILY REGULATORY PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00339; AA_TRNA_LIGASE_II_2; UNKNOWN_1.
PROSITE; PS01081; HTH_TETR_FAMILY; 1.
Complete proteome; DNA-binding; Transcription regulation
SEQUENCE 192 AA; 22259 MW; ED8BOB72A5FE6525 CRC64;
                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PRO0455; HTHTETR.

DNA-binding; Transcription regulation.

SEQUENCE 192 AA; 20940 MW; 54AEFDA6FF959E74 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-A3(2);
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19; Conserv
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    (TrEMBLrel.
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Streptomycineae; Streptomycetaceae; St
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Pred. No. 0.29
10; Mismatches
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EMBL/GenBank/DDBJ databa
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Pred. No. 0.14
10; Mismatches
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-!- SIMILARITY: TO THE TETR/ACRR FAMILY OF TRANSCRIPTION EMBL; AP001517; BAB06821.1; -
                                                                                                                                                                                                                                                                                                                  Q9HTJO;
                               MEDLINE-20437337; PubMed-10984043;
Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P. Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y. Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M. Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Firmicutes; Bacillus/Staphylococcus
NCBI_TaxID=86665;
           PRINTS; PR00455; HTHTETR PROSITE; PS01081; HTH_TET
                                                                                                                                                                                                                                        Pseudomonas aeruginosa.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                             01-MAR-2001
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complete
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MEDLINE=20512582; PubMed=11058132;
Takami H., Nakasone K., Takaki Y.,
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                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                    NCBI_TaxID=287;
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15; Conserv
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HTH_TETR_FAMILY; UNKNOWN_1; DNA-binding; Transcription
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Nakamura Y., O
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Pred. No. 0.29
22; Mismatches
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Ogasawara N.,
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Transcription

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Best Local S
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Mol. Microbiol. 21:77-96(1996).
-- SIMILARITY: TO THE TETR/ACRR FAMILY OF
EMBL; ALO96811; CAB46797.1; --
InterPro; IPR001647; HTH_TETR.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PUTATIVE TRANSCRIPTIONAL REGULATOR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA-binding; Transcription SEQUENCE 215 AA; 23123 M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN-A3(2);
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Submitted (JUL-1999)
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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SCI30A.20C.
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01-MAY-2000
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                                                                                                                                                                                                                                                                           DLASAVGTQSGSIFHHFKSKDETLRAVMEETIHYNTAMMRASLEEASTVRER----VLAL 56
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EMBL/GenBank/DDBJ databases.
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Pred. No. 0.38
16; Mismatches
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Pred. No. 0.47
22; Mismatches
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01-NOV-1999
01-NOV-1999
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Oliver K., Harris D.;
Oliver K., Harris D.;
"A set of ordered cosmids and a detailed genetic a
the 8 mb Streptomyces coelicolor A3(2) chromosome.
The 1 mb Streptomyces to the EMBL/GenBank/DDBJ data
                                                                                                                                                                                                                                 "A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome."; Mol. Microbiol. 21:77-96(1996).
-i- SIMILARITY: TO THE TETR/ACRR FAMILY OF TRANSCRIPTIONAL REGULATORS EMBL; AL049485; CAB39708.1; -.
InterPro; IPR001647; HTH_Tetr.
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SEQUENCE 206
                                                                                                                                                                                                                        Pfam; PF00440;
                                                                                                                                                                                                                                                                                                                                 MEDLINE=97000351; PubMed=8843436; Redenbach M., Kieser H.M., Denapaite D.,
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06 AA; 22344 MW; 75D88F30D7476A75 CRC64;
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